

SEQUENCE LISTING

<110> Hardiman, Gerard T.
 Rock, Fernando L.
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 Ho, Stephen W.K.
 Liu, Yong-Jun

<120> Human Receptor Proteins; Related Reagents and Methods

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<141> 2000-11-28

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<170> PatentIn Ver. 2.0

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Glu	Leu	Tyr	Ile	Ser	Arg	Asn	Lys	Leu	Met	Thr	Leu	Pro	Asp	Ala	Ser		

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ctc tta ccc atg tta cta gta ttg aaa atc agt agg aat gca ata act Leu Leu Pro Met Leu Leu Val Leu Lys Ile Ser Arg Asn Ala Ile Thr 475 480 485 490			1536
acg ttt tct aag gag caa ctt gac tca ttt cac aca ctg aag act ttg Thr Phe Ser Lys Glu Gln Leu Asp Ser Phe His Thr Leu Lys Thr Leu 495 500 505			1584
gaa gct ggt ggc aat aac ttc att tgc tcc tgt gaa ttc ctc tcc ttc Glu Ala Gly Gly Asn Asn Phe Ile Cys Ser Cys Glu Phe Leu Ser Phe 510 515 520			1632
act cag gag cag caa gca ctg gcc aaa gtc ttg att gat tgg cca gca Thr Gln Glu Gln Gln Ala Leu Ala Lys Val Leu Ile Asp Trp Pro Ala 525 530 535			1680
aat tac ctg tgt gac tct cca tcc cat gtg cgt ggc cag cag gtt cag Asn Tyr Leu Cys Asp Ser Pro Ser His Val Arg Gly Gln Gln Val Gln 540 545 550			1728
gat gtc cgc ctc tcg gtg tcg gaa tgt cac agg aca gca ctg gtg tct Asp Val Arg Leu Ser Val Ser Glu Cys His Arg Thr Ala Leu Val Ser 555 560 565 570			1776
ggc atg tgc tgt gct ctg ttc ctg ctg atc ctg ctc acg ggg gtc ctg Gly Met Cys Cys Ala Leu Phe Leu Leu Ile Leu Leu Thr Gly Val Leu 575 580 585			1824
tgc cac cgt ttc cat ggc ctg tgg tat atg aaa atg atg tgg gcc tgg Cys His Arg Phe His Gly Leu Trp Tyr Met Lys Met Met Trp Ala Trp 590 595 600			1872
ctc cag gcc aaa agg aag ccc agg aaa gct ccc agc agg aac atc tgc Leu Gln Ala Lys Arg Lys Pro Arg Lys Ala Pro Ser Arg Asn Ile Cys 605 610 615			1920
tat gat gca ttt gtt tct tac agt gag cgg gat gcc tac tgg gtg gag Tyr Asp Ala Phe Val Ser Tyr Ser Glu Arg Asp Ala Tyr Trp Val Glu 620 625 630			1968
aac ctt atg gtc cag gag ctg gag aac ttc aat ccc ccc ttc aag ttg Asn Leu Met Val Gln Glu Leu Glu Asn Phe Asn Pro Pro Phe Lys Leu 635 640 645 650			2016
tgt ctt cat aag cgg gac ttc att cct ggc aag tgg atc att gac aat Cys Leu His Lys Arg Asp Phe Ile Pro Gly Lys Trp Ile Ile Asp Asn 655 660 665			2064
atc att gac tcc att gaa aag agc cac aaa act gtc ttt gtg ctt tct Ile Ile Asp Ser Ile Glu Lys Ser His Lys Thr Val Phe Val Leu Ser 670 675 680			2112

gaa aac ttt gtg aag agt gag tgg tgc aag tat gaa ctg gac ttc tcc 2160
 Glu Asn Phe Val Lys Ser Glu Trp Cys Lys Tyr Glu Leu Asp Phe Ser
 685 690 695

cat ttc cgt ctt ttt gaa gag aac aat gat gct gcc att ctc att ctt 2208
 His Phe Arg Leu Phe Glu Glu Asn Asn Asp Ala Ala Ile Leu Ile Leu
 700 705 710

ctg gag ccc att gag aaa aaa gcc att ccc cag cgc ttc tgc aag ctg 2256
 Leu Glu Pro Ile Glu Lys Lys Ala Ile Pro Gln Arg Phe Cys Lys Leu
 715 720 725 730

cgg aag ata atg aac acc aag acc tac ctg gag tgg ccc atg gac gag 2304
 Arg Lys Ile Met Asn Thr Lys Thr Tyr Leu Glu Trp Pro Met Asp Glu
 735 740 745

gct cag cgg gaa gga ttt tgg gta aat ctg aga gct gcg ata aag tcc 2352
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Gly Leu Thr Glu Ala Val Lys Ser Leu Asp Leu Ser Asn Asn Arg Ile
 30 35 40

Thr Tyr Ile Ser Asn Ser Asp Leu Gln Arg Cys Val Asn Leu Gln Ala
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Leu Val Leu Thr Ser Asn Gly Ile Asn Thr Ile Glu Glu Asp Ser Phe
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Ser Ser Leu Gly Ser Leu Glu His Leu Asp Leu Ser Tyr Asn Tyr Leu
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Ser Asn Leu Ser Ser Ser Trp Phe Lys Pro Leu Ser Ser Leu Thr Phe
 95 100 105

Leu Asn Leu Leu Gly Asn Pro Tyr Lys Thr Leu Gly Glu Thr Ser Leu
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Phe Ser His Leu Thr Lys Leu Gln Ile Leu Arg Val Gly Asn Met Asp
 125 130 135

Thr Phe Thr Lys Ile Gln Arg Lys Asp Phe Ala Gly Leu Thr Phe Leu
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Glu Glu Leu Glu Ile Asp Ala Ser Asp Leu Gln Ser Tyr Glu Pro Lys
 155 160 165 170

Ser Leu Lys Ser Ile Gln Asn Val Ser His Leu Ile Leu His Met Lys
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Gln His Ile Leu Leu Leu Glu Ile Phe Val Asp Val Thr Ser Ser Val
 190 195 200

Glu Cys Leu Glu Leu Arg Asp Thr Asp Leu Asp Thr Phe His Phe Ser
 205 210 215

Glu Leu Ser Thr Gly Glu Thr Asn Ser Leu Ile Lys Lys Phe Thr Phe
 220 225 230

Arg Asn Val Lys Ile Thr Asp Glu Ser Leu Phe Gln Val Met Lys Leu
 235 240 245 250

Leu Asn Gln Ile Ser Gly Leu Leu Glu Leu Glu Phe Asp Asp Cys Thr
 255 260 265

Leu Asn Gly Val Gly Asn Phe Arg Ala Ser Asp Asn Asp Arg Val Ile
 270 275 280

Asp Pro Gly Lys Val Glu Thr Leu Thr Ile Arg Arg Leu His Ile Pro
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Arg Phe Tyr Leu Phe Tyr Asp Leu Ser Thr Leu Tyr Ser Leu Thr Glu
 300 305 310

Arg Val Lys Arg Ile Thr Val Glu Asn Ser Lys Val Phe Leu Val Pro
 315 320 325 330

Cys Leu Leu Ser Gln His Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser
 335 340 345

Glu Asn Leu Met Val Glu Glu Tyr Leu Lys Asn Ser Ala Cys Glu Asp
 350 355 360

Ala Trp Pro Ser Leu Gln Thr Leu Ile Leu Arg Gln Asn His Leu Ala
 365 370 375

Ser Leu Glu Lys Thr Gly Glu Thr Leu Leu Thr Leu Lys Asn Leu Thr
 380 385 390

Asn Ile Asp Ile Ser Lys Asn Ser Phe His Ser Met Pro Glu Thr Cys
 395 400 405 410
 Gln Trp Pro Glu Lys Met Lys Tyr Leu Asn Leu Ser Ser Thr Arg Ile
 415 420 425
 His Ser Val Thr Gly Cys Ile Pro Lys Thr Leu Glu Ile Leu Asp Val
 430 435 440
 Ser Asn Asn Asn Leu Asn Leu Phe Ser Leu Asn Leu Pro Gln Leu Lys
 445 450 455
 Glu Leu Tyr Ile Ser Arg Asn Lys Leu Met Thr Leu Pro Asp Ala Ser
 460 465 470
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 475 480 485 490
 Thr Phe Ser Lys Glu Gln Leu Asp Ser Phe His Thr Leu Lys Thr Leu
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 Glu Ala Gly Gly Asn Asn Phe Ile Cys Ser Cys Glu Phe Leu Ser Phe
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 Thr Gln Glu Gln Gln Ala Leu Ala Lys Val Leu Ile Asp Trp Pro Ala
 525 530 535
 Asn Tyr Leu Cys Asp Ser Pro Ser His Val Arg Gly Gln Gln Val Gln
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 Asp Val Arg Leu Ser Val Ser Glu Cys His Arg Thr Ala Leu Val Ser
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 Gly Met Cys Cys Ala Leu Phe Leu Leu Ile Leu Leu Thr Gly Val Leu
 575 580 585
 Cys His Arg Phe His Gly Leu Trp Tyr Met Lys Met Met Trp Ala Trp
 590 595 600
 Leu Gln Ala Lys Arg Lys Pro Arg Lys Ala Pro Ser Arg Asn Ile Cys
 605 610 615
 Tyr Asp Ala Phe Val Ser Tyr Ser Glu Arg Asp Ala Tyr Trp Val Glu
 620 625 630
 Asn Leu Met Val Gln Glu Leu Glu Asn Phe Asn Pro Pro Phe Lys Leu
 635 640 645 650
 Cys Leu His Lys Arg Asp Phe Ile Pro Gly Lys Trp Ile Ile Asp Asn
 655 660 665
 Ile Ile Asp Ser Ile Glu Lys Ser His Lys Thr Val Phe Val Leu Ser
 670 675 680

Glu Asn Phe Val Lys Ser Glu Trp Cys Lys Tyr Glu Leu Asp Phe Ser
685 690 695

His Phe Arg Leu Phe Glu Glu Asn Asn Asp Ala Ala Ile Leu Ile Leu
700 705 710

Leu Glu Pro Ile Glu Lys Lys Ala Ile Pro Gln Arg Phe Cys Lys Leu
715 720 725 730

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Homo sapiens

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Phe Gly Met Leu Cys Ala Ser Ser Thr Thr Lys Cys Thr Val Ser His
-5 -1 1 5 10

gaa gtt gct gac tgc agc cac ctg aag ttg act cag gta ccc gat gat 144
Glu Val Ala Asp Cys Ser His Leu Lys Leu Thr Gln Val Pro Asp Asp
15 20 25

cta ccc aca aac ata aca gtg ttg aac ctt acc cat aat caa ctc aga 192
Leu Pro Thr Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu Arg
30 35 40

aga tta cca gcc gcc aac ttc aca agg tat agc cag cta act agc ttg 240
Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu
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Asp	Val	Gly	Phe	Asn	Thr	Ile	Ser	Lys	Leu	Glu	Pro	Glu	Leu	Cys	Gln	
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aaa	ctt	ccc	atg	tta	aaa	gtt	ttg	aac	ctc	cag	cac	aat	gag	cta	tct	336
Lys	Leu	Pro	Met	Leu	Lys	Val	Leu	Asn	Leu	Gln	His	Asn	Glu	Leu	Ser	
				80					85						90	
caa	ctt	tct	gat	aaa	acc	ttt	gcc	ttc	tgc	acg	aat	ttg	act	gaa	ctc	384
Gln	Leu	Ser	Asp	Lys	Thr	Phe	Ala	Phe	Cys	Thr	Asn	Leu	Thr	Glu	Leu	
			95					100					105			
cat	ctc	atg	tcc	aac	tca	atc	cag	aaa	att	aaa	aat	aat	ccc	ttt	gtc	432
His	Leu	Met	Ser	Asn	Ser	Ile	Gln	Lys	Ile	Lys	Asn	Asn	Pro	Phe	Val	
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Lys	Gln	Lys	Asn	Leu	Ile	Thr	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu	Ser	
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tct	aca	aaa	tta	gga	act	cag	gtt	cag	ctg	gaa	aat	ctc	caa	gag	ctt	528
Ser	Thr	Lys	Leu	Gly	Thr	Gln	Val	Gln	Leu	Glu	Asn	Leu	Gln	Glu	Leu	
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Leu	Leu	Ser	Asn	Asn	Lys	Ile	Gln	Ala	Leu	Lys	Ser	Glu	Glu	Leu	Asp	
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Ile	Phe	Ala	Asn	Ser	Ser	Leu	Lys	Lys	Leu	Glu	Leu	Ser	Ser	Asn	Gln	
			175					180					185			
att	aaa	gag	ttt	tct	cca	ggg	tgt	ttt	cac	gca	att	gga	aga	tta	ttt	672
Ile	Lys	Glu	Phe	Ser	Pro	Gly	Cys	Phe	His	Ala	Ile	Gly	Arg	Leu	Phe	
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ggc	ctc	ttt	ctg	aac	aat	gtc	cag	ctg	ggc	ccc	agc	ctt	aca	gag	aag	720
Gly	Leu	Phe	Leu	Asn	Asn	Val	Gln	Leu	Gly	Pro	Ser	Leu	Thr	Glu	Lys	
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Leu	Cys	Leu	Glu	Leu	Ala	Asn	Thr	Ser	Ile	Arg	Asn	Leu	Ser	Leu	Ser	
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aac	agc	cag	ctg	tcc	acc	acc	agc	aat	aca	act	ttc	ttg	gga	cta	aag	816
Asn	Ser	Gln	Leu	Ser	Thr	Thr	Ser	Asn	Thr	Thr	Phe	Leu	Gly	Leu	Lys	
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tgg	aca	aat	ctc	act	atg	ctc	gat	ctt	tcc	tac	aac	aac	tta	aat	gtg	864
Trp	Thr	Asn	Leu	Thr	Met	Leu	Asp	Leu	Ser	Tyr	Asn	Asn	Leu	Asn	Val	
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gtt ggt aac gat tcc ttt gct tgg ctt cca caa cta gaa tat ttc ttc	912
Val Gly Asn Asp Ser Phe Ala Trp Leu Pro Gln Leu Glu Tyr Phe Phe	
270 275 280	
cta gag tat aat aat ata cag cat ttg ttt tct cac tct ttg cac ggg	960
Leu Glu Tyr Asn Asn Ile Gln His Leu Phe Ser His Ser Leu His Gly	
285 290 295	
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Leu Phe Asn Val Arg Tyr Leu Asn Leu Lys Arg Ser Phe Thr Lys Gln	
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agt att tcc ctt gcc tca ctc ccc aag att gat gat ttt tct ttt cag	1056
Ser Ile Ser Leu Ala Ser Leu Pro Lys Ile Asp Asp Phe Ser Phe Gln	
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Trp Leu Lys Cys Leu Glu His Leu Asn Met Glu Asp Asn Asp Ile Pro	
335 340 345	
ggc ata aaa agc aat atg ttc aca gga ttg ata aac ctg aaa tac tta	1152
Gly Ile Lys Ser Asn Met Phe Thr Gly Leu Ile Asn Leu Lys Tyr Leu	
350 355 360	
agg cta tcc aac tcc ttt aca agt ttg cga act ttg aca aat gaa aca	1200
Ser Leu Ser Asn Ser Phe Thr Ser Leu Arg Thr Leu Thr Asn Glu Thr	
365 370 375	
ttt gta tca ctt gct cat tct ccc tta cac ata ctc aac cta acc aag	1248
Phe Val Ser Leu Ala His Ser Pro Leu His Ile Leu Asn Leu Thr Lys	
380 385 390 395	
aat aaa atc tca aaa ata gag agt gat gct ttc tct tgg ttg ggc cac	1296
Asn Lys Ile Ser Lys Ile Glu Ser Asp Ala Phe Ser Trp Leu Gly His	
400 405 410	
cta gaa gta ctt gac ctg ggc ctt aat gaa att ggg caa gaa ctc aca	1344
Leu Glu Val Leu Asp Leu Gly Leu Asn Glu Ile Gly Gln Glu Leu Thr	
415 420 425	
ggc cag gaa tgg aga ggt cta gaa aat att ttc gaa atc tat ctt tcc	1392
Gly Gln Glu Trp Arg Gly Leu Glu Asn Ile Phe Glu Ile Tyr Leu Ser	
430 435 440	
tac aac aag tac ctg cag ctg act agg aac tcc ttt gcc ttg gtc cca	1440
Tyr Asn Lys Tyr Leu Gln Leu Thr Arg Asn Ser Phe Ala Leu Val Pro	
445 450 455	
agc ctt caa cga ctg atg ctc cga agg gtg gcc ctt aaa aat gtg gat	1488
Ser Leu Gln Arg Leu Met Leu Arg Arg Val Ala Leu Lys Asn Val Asp	
460 465 470 475	
agc tct cct tca cca ttc cag cct ctt cgt aac ttg acc att ctg gat	1536
Ser Ser Pro Ser Pro Phe Gln Pro Leu Arg Asn Leu Thr Ile Leu Asp	

480										485					490					
cta	agc	aac	aac	aac	ata	gcc	aac	ata	aat	gat	gac	atg	ttg	gag	ggt	1584				
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Leu	Glu	Lys	Leu	Glu	Ile	Leu	Asp	Leu	Gln	His	Asn	Asn	Leu	Ala	Arg					
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Leu	Trp	Lys	His	Ala	Asn	Pro	Gly	Gly	Pro	Ile	Tyr	Phe	Leu	Lys	Gly					
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Leu	Ser	His	Leu	His	Ile	Leu	Asn	Leu	Glu	Ser	Asn	Gly	Phe	Asp	Glu					
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atc	cca	ggt	gag	gtc	ttc	aag	gat	tta	ttt	gaa	cta	aag	atc	atc	gat	1776				
Ile	Pro	Val	Glu	Val	Phe	Lys	Asp	Leu	Phe	Glu	Leu	Lys	Ile	Ile	Asp					
				560					565					570						
tta	gga	ttg	aat	aat	tta	aac	aca	ctt	cca	gca	tct	gtc	ttt	aat	aat	1824				
Leu	Gly	Leu	Asn	Asn	Leu	Asn	Thr	Leu	Pro	Ala	Ser	Val	Phe	Asn	Asn					
			575					580					585							
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Gln	Val	Ser	Leu	Lys	Ser	Leu	Asn	Leu	Gln	Lys	Asn	Leu	Ile	Thr	Ser					
		590					595					600								
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gat	atg	cgc	ttt	aat	ccc	ttt	gat	tgc	acg	tgt	gaa	agt	att	gcc	tgg	1968				
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ttt	ggt	aat	tgg	att	aac	gag	acc	cat	acc	aac	atc	cct	gag	ctg	tca	2016				
Phe	Val	Asn	Trp	Ile	Asn	Glu	Thr	His	Thr	Asn	Ile	Pro	Glu	Leu	Ser					
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Ser	His	Tyr	Leu	Cys	Asn	Thr	Pro	Pro	His	Tyr	His	Gly	Phe	Pro	Val					
			655					660					665							
aga	ctt	ttt	gat	aca	tca	tct	tgc	aaa	gac	agt	gcc	ccc	ttt	gaa	ctc	2112				
Arg	Leu	Phe	Asp	Thr	Ser	Ser	Cys	Lys	Asp	Ser	Ala	Pro	Phe	Glu	Leu					
		670					675					680								
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Phe	Phe	Met	Ile	Asn	Thr	Ser	Ile	Leu	Leu	Ile	Phe	Ile	Phe	Ile	Val					
		685					690				695									

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cag ttt gaa tat gca gca tat ata att cat gcc tat aaa gat aag gat Gln Phe Glu Tyr Ala Ala Tyr Ile Ile His Ala Tyr Lys Asp Lys Asp 735 740 745	2304
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gaa gca att gtt aac agc atc aaa aga agc aga aaa att att ttt gtt Glu Ala Ile Val Asn Ser Ile Lys Arg Ser Arg Lys Ile Ile Phe Val 780 785 790 795	2448
aca cac cat cta tta aaa gac cca tta tgc aaa aga ttc aag gta Ile Thr His His Leu Leu Lys Asp Pro Leu Cys Lys Arg Phe Lys Val 800 805 810	2496
cat cat gca gtt caa caa gct att gaa caa aat ctg gat tcc att ata His His Ala Val Gln Gln Ala Ile Glu Gln Asn Leu Asp Ser Ile Ile 815 820 825	2544
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Leu Pro Thr Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu Arg
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Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu
45 50 55

Asp Val Gly Phe Asn Thr Ile Ser Lys Leu Glu Pro Glu Leu Cys Gln
60 65 70 75

Lys Leu Pro Met Leu Lys Val Leu Asn Leu Gln His Asn Glu Leu Ser
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Gln Leu Ser Asp Lys Thr Phe Ala Phe Cys Thr Asn Leu Thr Glu Leu
95 100 105

His Leu Met Ser Asn Ser Ile Gln Lys Ile Lys Asn Asn Pro Phe Val
110 115 120

Lys Gln Lys Asn Leu Ile Thr Leu Asp Leu Ser His Asn Gly Leu Ser
125 130 135

Ser Thr Lys Leu Gly Thr Gln Val Gln Leu Glu Asn Leu Gln Glu Leu
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Leu Leu Ser Asn Asn Lys Ile Gln Ala Leu Lys Ser Glu Glu Leu Asp
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Ile Phe Ala Asn Ser Ser Leu Lys Lys Leu Glu Leu Ser Ser Asn Gln
175 180 185

Ile Lys Glu Phe Ser Pro Gly Cys Phe His Ala Ile Gly Arg Leu Phe
190 195 200

Gly Leu Phe Leu Asn Asn Val Gln Leu Gly Pro Ser Leu Thr Glu Lys
205 210 215

Leu Cys Leu Glu Leu Ala Asn Thr Ser Ile Arg Asn Leu Ser Leu Ser
220 225 230 235

Asn Ser Gln Leu Ser Thr Thr Ser Asn Thr Thr Phe Leu Gly Leu Lys
240 245 250

Trp Thr Asn Leu Thr Met Leu Asp Leu Ser Tyr Asn Asn Leu Asn Val
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 Val Gly Asn Asp Ser Phe Ala Trp Leu Pro Gln Leu Glu Tyr Phe Phe
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 Leu Glu Tyr Asn Asn Ile Gln His Leu Phe Ser His Ser Leu His Gly
 285 290 295
 Leu Phe Asn Val Arg Tyr Leu Asn Leu Lys Arg Ser Phe Thr Lys Gln
 300 305 310 315
 Ser Ile Ser Leu Ala Ser Leu Pro Lys Ile Asp Asp Phe Ser Phe Gln
 320 325 330
 Trp Leu Lys Cys Leu Glu His Leu Asn Met Glu Asp Asn Asp Ile Pro
 335 340 345
 Gly Ile Lys Ser Asn Met Phe Thr Gly Leu Ile Asn Leu Lys Tyr Leu
 350 355 360
 Ser Leu Ser Asn Ser Phe Thr Ser Leu Arg Thr Leu Thr Asn Glu Thr
 365 370 375
 Phe Val Ser Leu Ala His Ser Pro Leu His Ile Leu Asn Leu Thr Lys
 380 385 390 395
 Asn Lys Ile Ser Lys Ile Glu Ser Asp Ala Phe Ser Trp Leu Gly His
 400 405 410
 Leu Glu Val Leu Asp Leu Gly Leu Asn Glu Ile Gly Gln Glu Leu Thr
 415 420 425
 Gly Gln Glu Trp Arg Gly Leu Glu Asn Ile Phe Glu Ile Tyr Leu Ser
 430 435 440
 Tyr Asn Lys Tyr Leu Gln Leu Thr Arg Asn Ser Phe Ala Leu Val Pro
 445 450 455
 Ser Leu Gln Arg Leu Met Leu Arg Arg Val Ala Leu Lys Asn Val Asp
 460 465 470 475
 Ser Ser Pro Ser Pro Phe Gln Pro Leu Arg Asn Leu Thr Ile Leu Asp
 480 485 490
 Leu Ser Asn Asn Asn Ile Ala Asn Ile Asn Asp Asp Met Leu Glu Gly
 495 500 505
 Leu Glu Lys Leu Glu Ile Leu Asp Leu Gln His Asn Asn Leu Ala Arg
 510 515 520
 Leu Trp Lys His Ala Asn Pro Gly Gly Pro Ile Tyr Phe Leu Lys Gly
 525 530 535

Leu Ser His Leu His Ile Leu Asn Leu Glu Ser Asn Gly Phe Asp Glu
 540 545 550 555
 Ile Pro Val Glu Val Phe Lys Asp Leu Phe Glu Leu Lys Ile Ile Asp
 560 565 570
 Leu Gly Leu Asn Asn Leu Asn Thr Leu Pro Ala Ser Val Phe Asn Asn
 575 580 585
 Gln Val Ser Leu Lys Ser Leu Asn Leu Gln Lys Asn Leu Ile Thr Ser
 590 595 600
 Val Glu Lys Lys Val Phe Gly Pro Ala Phe Arg Asn Leu Thr Glu Leu
 605 610 615
 Asp Met Arg Phe Asn Pro Phe Asp Cys Thr Cys Glu Ser Ile Ala Trp
 620 625 630 635
 Phe Val Asn Trp Ile Asn Glu Thr His Thr Asn Ile Pro Glu Leu Ser
 640 645 650
 Ser His Tyr Leu Cys Asn Thr Pro Pro His Tyr His Gly Phe Pro Val
 655 660 665
 Arg Leu Phe Asp Thr Ser Ser Cys Lys Asp Ser Ala Pro Phe Glu Leu
 670 675 680
 Phe Phe Met Ile Asn Thr Ser Ile Leu Leu Ile Phe Ile Phe Ile Val
 685 690 695
 Leu Leu Ile His Phe Glu Gly Trp Arg Ile Ser Phe Tyr Trp Asn Val
 700 705 710 715
 Ser Val His Arg Val Leu Gly Phe Lys Glu Ile Asp Arg Gln Thr Glu
 720 725 730
 Gln Phe Glu Tyr Ala Ala Tyr Ile Ile His Ala Tyr Lys Asp Lys Asp
 735 740 745
 Trp Val Trp Glu His Phe Ser Ser Met Glu Lys Glu Asp Gln Ser Leu
 750 755 760
 Lys Phe Cys Leu Glu Glu Arg Asp Phe Glu Ala Gly Val Phe Glu Leu
 765 770 775
 Glu Ala Ile Val Asn Ser Ile Lys Arg Ser Arg Lys Ile Ile Phe Val
 780 785 790 795
 Ile Thr His His Leu Leu Lys Asp Pro Leu Cys Lys Arg Phe Lys Val
 800 805 810
 His His Ala Val Gln Gln Ala Ile Glu Gln Asn Leu Asp Ser Ile Ile
 815 820 825

Leu Val Phe Leu Glu Glu Ile Pro Asp Tyr Lys Leu Asn His Ala Leu
 830 835 840

Cys Leu Arg Arg Gly Met Phe Lys Ser His Cys Ile Leu Asn Trp Pro
 845 850 855

Val Gln Lys Glu Arg Ile Gly Ala Phe Arg His Lys Leu Gln Val Ala
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Leu Gly Ser Lys Asn Ser Val His
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<223> Description of Unknown Organism: primate; surmised
 Homo sapiens

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<221> CDS

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aag aac ctg gac ctg agc ttt aat ccc ctg agg cat tta ggc agc tat 96
 Lys Asn Leu Asp Leu Ser Phe Asn Pro Leu Arg His Leu Gly Ser Tyr
 20 25 30

agc ttc ttc agt ttc cca gaa ctg cag gtg ctg gat tta tcc agg tgt 144
 Ser Phe Phe Ser Phe Pro Glu Leu Gln Val Leu Asp Leu Ser Arg Cys
 35 40 45

gaa atc cag aca att gaa gat ggg gca tat cag agc cta agc cac ctc 192
 Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr Gln Ser Leu Ser His Leu
 50 55 60

tct acc tta ata ttg aca gga aac ccc atc cag agt tta gcc ctg gga 240
 Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile Gln Ser Leu Ala Leu Gly
 65 70 75 80

gcc ttt tct gga cta tca agt tta cag aag ctg gtg gct gtg gag aca 288
 Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala Val Glu Thr
 85 90 95

aat cta gca tct cta gag aac ttc ccc att gga cat ctc aaa act ttg 336
 Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile Gly His Leu Lys Thr Leu

100										105					110					
aaa gaa ctt aat gtg gct cac aat ctt atc caa tct ttc aaa tta cct	384																			
Lys Glu Leu Asn Val Ala His Asn Leu Ile Gln Ser Phe Lys Leu Pro																				
115 120 125																				
gag tat ttt tct aat ctg acc aat cta gag cac ttg gac ctt tcc agc	432																			
Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu His Leu Asp Leu Ser Ser																				
130 135 140																				
aac aag att caa agt att tat tgc aca gac ttg cgg gtt cta cat caa	480																			
Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp Leu Arg Val Leu His Gln																				
145 150 155 160																				
atg ccc cta ctc aat ctc tct tta gac ctg tcc ctg aac cct atg aac	528																			
Met Pro Leu Leu Asn Leu Ser Leu Asp Leu Ser Leu Asn Pro Met Asn																				
165 170 175																				
ttt atc caa cca ggt gca ttt aaa gaa att agg ctt cat aag ctg act	576																			
Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu His Lys Leu Thr																				
180 185 190																				
tta aga aat aat ttt gat agt tta aat gta atg aaa act tgt att caa	624																			
Leu Arg Asn Asn Phe Asp Ser Leu Asn Val Met Lys Thr Cys Ile Gln																				
195 200 205																				
ggg ctg gct ggt tta gaa gtc cat cgt ttg gtt ctg gga gaa ttt aga	672																			
Gly Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly Glu Phe Arg																				
210 215 220																				
aat gaa gga aac ttg gaa aag ttt gac aaa tct gct cta gag ggc ctg	720																			
Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys Ser Ala Leu Glu Gly Leu																				
225 230 235 240																				
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Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr																				
245 250 255																				
ctc gat gat att att gac tta ttt aat tgt ttg aca aat gtt tct tca	816																			
Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Thr Asn Val Ser Ser																				
260 265 270																				
ttt tcc ctg gtg agt gtg act att gaa agg gta aaa gac ttt tct tat	864																			
Phe Ser Leu Val Ser Val Thr Ile Glu Arg Val Lys Asp Phe Ser Tyr																				
275 280 285																				
aat ttc gga tgg caa cat tta gaa tta gtt aac tgt aaa ttt gga cag	912																			
Asn Phe Gly Trp Gln His Leu Glu Leu Val Asn Cys Lys Phe Gly Gln																				
290 295 300																				
ttt ccc aca ttg aaa ctc aaa tct ctc aaa agg ctt act ttc act tcc	960																			
Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr Phe Thr Ser																				
305 310 315 320																				

aac	aaa	ggg	ggg	aat	gct	ttt	tca	gaa	gtt	gat	cta	cca	agc	ctt	gag	1008
Asn	Lys	Gly	Gly	Asn	Ala	Phe	Ser	Glu	Val	Asp	Leu	Pro	Ser	Leu	Glu	
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ttt	cta	gat	ctc	agt	aga	aat	ggc	ttg	agt	ttc	aaa	ggg	tgc	tgt	tct	1056
Phe	Leu	Asp	Leu	Ser	Arg	Asn	Gly	Leu	Ser	Phe	Lys	Gly	Cys	Cys	Ser	
			340					345					350			
caa	agt	gat	ttt	ggg	aca	acc	agc	cta	aag	tat	tta	gat	ctg	agc	ttc	1104
Gln	Ser	Asp	Phe	Gly	Thr	Thr	Ser	Leu	Lys	Tyr	Leu	Asp	Leu	Ser	Phe	
		355					360					365				
aat	ggg	gtt	att	acc	atg	agt	tca	aac	ttc	ttg	ggc	tta	gaa	caa	cta	1152
Asn	Gly	Val	Ile	Thr	Met	Ser	Ser	Asn	Phe	Leu	Gly	Leu	Glu	Gln	Leu	
	370					375					380					
gaa	cat	ctg	gat	ttc	cag	cat	tcc	aat	ttg	aaa	caa	atg	agt	gag	ttt	1200
Glu	His	Leu	Asp	Phe	Gln	His	Ser	Asn	Leu	Lys	Gln	Met	Ser	Glu	Phe	
385					390					395					400	
tca	gta	ttc	cta	tca	ctc	aga	aac	ctc	att	tac	ctt	gac	att	tct	cat	1248
Ser	Val	Phe	Leu	Ser	Leu	Arg	Asn	Leu	Ile	Tyr	Leu	Asp	Ile	Ser	His	
				405					410					415		
acc	cac	acc	aga	gtt	gct	ttc	aat	ggc	atc	ttc	aat	ggc	ttg	tcc	agt	1296
Thr	His	Thr	Arg	Val	Ala	Phe	Asn	Gly	Ile	Phe	Asn	Gly	Leu	Ser	Ser	
			420					425					430			
ctc	gaa	gtc	ttg	aaa	atg	gct	ggc	aat	tct	ttc	cag	gaa	aac	ttc	ctt	1344
Leu	Glu	Val	Leu	Lys	Met	Ala	Gly	Asn	Ser	Phe	Gln	Glu	Asn	Phe	Leu	
		435					440					445				
cca	gat	atc	ttc	aca	gag	ctg	aga	aac	ttg	acc	ttc	ctg	gac	ctc	tct	1392
Pro	Asp	Ile	Phe	Thr	Glu	Leu	Arg	Asn	Leu	Thr	Phe	Leu	Asp	Leu	Ser	
	450					455					460					
cag	tgt	caa	ctg	gag	cag	ttg	tct	cca	aca	gca	ttt	aac	tca	ctc	tcc	1440
Gln	Cys	Gln	Leu	Glu	Gln	Leu	Ser	Pro	Thr	Ala	Phe	Asn	Ser	Leu	Ser	
465					470					475					480	
agt	ctt	cag	gta	cta	aat	atg	agc	cac	aac	aac	ttc	ttt	tca	ttg	gat	1488
Ser	Leu	Gln	Val	Leu	Asn	Met	Ser	His	Asn	Asn	Phe	Phe	Ser	Leu	Asp	
				485					490					495		
acg	ttt	cct	tat	aag	tgt	ctg	aac	tcc	ctc	cag	gtt	ctt	gat	tac	agt	1536
Thr	Phe	Pro	Tyr	Lys	Cys	Leu	Asn	Ser	Leu	Gln	Val	Leu	Asp	Tyr	Ser	
			500					505					510			
ctc	aat	cac	ata	atg	act	tcc	aaa	aaa	cag	gaa	cta	cag	cat	ttt	cca	1584
Leu	Asn	His	Ile	Met	Thr	Ser	Lys	Lys	Gln	Glu	Leu	Gln	His	Phe	Pro	
		515					520					525				
agt	agt	cta	gct	ttc	tta	aat	ctt	act	cag	aat	gac	ttt	gct	tgt	act	1632

Ser	Ser	Leu	Ala	Phe	Leu	Asn	Leu	Thr	Gln	Asn	Asp	Phe	Ala	Cys	Thr		
530						535					540						
tgt	gaa	cac	cag	agt	ttc	ctg	caa	tgg	atc	aag	gac	cag	agg	cag	ctc	1680	
Cys	Glu	His	Gln	Ser	Phe	Leu	Gln	Trp	Ile	Lys	Asp	Gln	Arg	Gln	Leu		
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ttg	gtg	gaa	gtt	gaa	cga	atg	gaa	tgt	gca	aca	cct	tca	gat	aag	cag	1728	
Leu	Val	Glu	Val	Glu	Arg	Met	Glu	Cys	Ala	Thr	Pro	Ser	Asp	Lys	Gln		
				565					570					575			
ggc	atg	cct	gtg	ctg	agt	ttg	aat	atc	acc	tgt	cag	atg	aat	aag	acc	1776	
Gly	Met	Pro	Val	Leu	Ser	Leu	Asn	Ile	Thr	Cys	Gln	Met	Asn	Lys	Thr		
			580					585					590				
atc	att	ggc	gtg	tcg	gtc	ctc	agt	gtg	ctt	gta	gta	tct	gtt	gta	gca	1824	
Ile	Ile	Gly	Val	Ser	Val	Leu	Ser	Val	Leu	Val	Val	Ser	Val	Val	Ala		
		595					600					605					
gtt	ctg	gtc	tat	aag	ttc	tat	ttt	cac	ctg	atg	ctt	ctt	gct	ggc	tgc	1872	
Val	Leu	Val	Tyr	Lys	Phe	Tyr	Phe	His	Leu	Met	Leu	Leu	Ala	Gly	Cys		
			610			615					620						
ata	aag	tat	ggc	aga	ggc	gaa	aac	atc	tat	gat	gcc	ttt	gtt	atc	tac	1920	
Ile	Lys	Tyr	Gly	Arg	Gly	Glu	Asn	Ile	Tyr	Asp	Ala	Phe	Val	Ile	Tyr		
625					630					635					640		
tea	agc	cag	gat	gag	gac	tgg	gta	agg	aat	gag	cta	gta	aag	aat	tta	1968	
Ser	Ser	Gln	Asp	Glu	Asp	Trp	Val	Arg	Asn	Glu	Leu	Val	Lys	Asn	Leu		
				645					650					655			
gaa	gaa	ggg	gtg	cct	cca	ttt	cag	ctc	tgc	ctt	cac	tac	aga	gac	ttt	2016	
Glu	Glu	Gly	Val	Pro	Pro	Phe	Gln	Leu	Cys	Leu	His	Tyr	Arg	Asp	Phe		
			660					665					670				
att	ccc	ggc	gtg	gcc	att	gct	gcc	aac	atc	atc	cat	gaa	ggc	ttc	cat	2064	
Ile	Pro	Gly	Val	Ala	Ile	Ala	Ala	Asn	Ile	Ile	His	Glu	Gly	Phe	His		
		675					680					685					
aaa	agc	cga	aag	gtg	att	gtt	gtg	gtg	tcc	cag	cac	ttc	atc	cag	agc	2112	
Lys	Ser	Arg	Lys	Val	Ile	Val	Val	Val	Ser	Gln	His	Phe	Ile	Gln	Ser		
						695					700						
cgc	tgg	tgt	atc	ttt	gaa	tat	gag	att	gct	cag	acc	tgg	cag	ttt	ctg	2160	
Arg	Trp	Cys	Ile	Phe	Glu	Tyr	Glu	Ile	Ala	Gln	Thr	Trp	Gln	Phe	Leu		
705					710					715					720		
agc	agt	cgt	gct	ggc	atc	atc	ttc	att	gtc	ctg	cag	aag	gtg	gag	aag	2208	
Ser	Ser	Arg	Ala	Gly	Ile	Ile	Phe	Ile	Val	Leu	Gln	Lys	Val	Glu	Lys		
				725					730					735			
acc	ctg	ctc	agg	cag	cag	gtg	gag	ctg	tac	cgc	ctt	ctc	agc	agg	aac	2256	
Thr	Leu	Leu	Arg	Gln	Gln	Val	Glu	Leu	Tyr	Arg	Leu	Leu	Ser	Arg	Asn		

740

745

750

act tac ctg gag tgg gag gac agt gtc ctg ggg cgg cac atc ttc tgg 2304
 Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu Gly Arg His Ile Phe Trp
 755 760 765

aga cga ctc aga aaa gcc ctg ctg gat ggt aaa tca tgg aat cca gaa 2352
 Arg Arg Leu Arg Lys Ala Leu Leu Asp Gly Lys Ser Trp Asn Pro Glu
 770 775 780

gga aca gtg ggt aca gga tgc aat tgg cag gaa gca aca tct atc tga 2400
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Ser Phe Phe Ser Phe Pro Glu Leu Gln Val Leu Asp Leu Ser Arg Cys
 35 40 45

Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr Gln Ser Leu Ser His Leu
 50 55 60

Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile Gln Ser Leu Ala Leu Gly
 65 70 75 80

Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala Val Glu Thr
 85 90 95

Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile Gly His Leu Lys Thr Leu
 100 105 110

Lys Glu Leu Asn Val Ala His Asn Leu Ile Gln Ser Phe Lys Leu Pro
 115 120 125

Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu His Leu Asp Leu Ser Ser
 130 135 140

Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp Leu Arg Val Leu His Gln
 145 150 155 160

Met Pro Leu Leu Asn Leu Ser Leu Asp Leu Ser Leu Asn Pro Met Asn
 165 170 175

Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu His Lys Leu Thr
180 185 190
Leu Arg Asn Asn Phe Asp Ser Leu Asn Val Met Lys Thr Cys Ile Gln
195 200 205
Gly Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly Glu Phe Arg
210 215 220
Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys Ser Ala Leu Glu Gly Leu
225 230 235 240
Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr
245 250 255
Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Thr Asn Val Ser Ser
260 265 270
Phe Ser Leu Val Ser Val Thr Ile Glu Arg Val Lys Asp Phe Ser Tyr
275 280 285
Asn Phe Gly Trp Gln His Leu Glu Leu Val Asn Cys Lys Phe Gly Gln
290 295 300
Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr Phe Thr Ser
305 310 315 320
Asn Lys Gly Gly Asn Ala Phe Ser Glu Val Asp Leu Pro Ser Leu Glu
325 330 335
Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser Phe Lys Gly Cys Cys Ser
340 345 350
Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys Tyr Leu Asp Leu Ser Phe
355 360 365
Asn Gly Val Ile Thr Met Ser Ser Asn Phe Leu Gly Leu Glu Gln Leu
370 375 380
Glu His Leu Asp Phe Gln His Ser Asn Leu Lys Gln Met Ser Glu Phe
385 390 395 400
Ser Val Phe Leu Ser Leu Arg Asn Leu Ile Tyr Leu Asp Ile Ser His
405 410 415
Thr His Thr Arg Val Ala Phe Asn Gly Ile Phe Asn Gly Leu Ser Ser
420 425 430
Leu Glu Val Leu Lys Met Ala Gly Asn Ser Phe Gln Glu Asn Phe Leu
435 440 445
Pro Asp Ile Phe Thr Glu Leu Arg Asn Leu Thr Phe Leu Asp Leu Ser
450 455 460

Gln Cys Gln Leu Glu Gln Leu Ser Pro Thr Ala Phe Asn Ser Leu Ser
 465 470 475 480
 Ser Leu Gln Val Leu Asn Met Ser His Asn Asn Phe Phe Ser Leu Asp
 485 490 495
 Thr Phe Pro Tyr Lys Cys Leu Asn Ser Leu Gln Val Leu Asp Tyr Ser
 500 505 510
 Leu Asn His Ile Met Thr Ser Lys Lys Gln Glu Leu Gln His Phe Pro
 515 520 525
 Ser Ser Leu Ala Phe Leu Asn Leu Thr Gln Asn Asp Phe Ala Cys Thr
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 Cys Glu His Gln Ser Phe Leu Gln Trp Ile Lys Asp Gln Arg Gln Leu
 545 550 555 560
 Leu Val Glu Val Glu Arg Met Glu Cys Ala Thr Pro Ser Asp Lys Gln
 565 570 575
 Gly Met Pro Val Leu Ser Leu Asn Ile Thr Cys Gln Met Asn Lys Thr
 580 585 590
 Ile Ile Gly Val Ser Val Leu Ser Val Leu Val Val Ser Val Val Ala
 595 600 605
 Val Leu Val Tyr Lys Phe Tyr Phe His Leu Met Leu Leu Ala Gly Cys
 610 615 620
 Ile Lys Tyr Gly Arg Gly Glu Asn Ile Tyr Asp Ala Phe Val Ile Tyr
 625 630 635 640
 Ser Ser Gln Asp Glu Asp Trp Val Arg Asn Glu Leu Val Lys Asn Leu
 645 650 655
 Glu Glu Gly Val Pro Pro Phe Gln Leu Cys Leu His Tyr Arg Asp Phe
 660 665 670
 Ile Pro Gly Val Ala Ile Ala Ala Asn Ile Ile His Glu Gly Phe His
 675 680 685
 Lys Ser Arg Lys Val Ile Val Val Val Ser Gln His Phe Ile Gln Ser
 690 695 700
 Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala Gln Thr Trp Gln Phe Leu
 705 710 715 720
 Ser Ser Arg Ala Gly Ile Ile Phe Ile Val Leu Gln Lys Val Glu Lys
 725 730 735
 Thr Leu Leu Arg Gln Gln Val Glu Leu Tyr Arg Leu Leu Ser Arg Asn
 740 745 750

Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu Gly Arg His Ile Phe Trp
 755 760 765

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 Homo sapiens

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 aat cat aac tat ctt aat tcc ctt cca cca gga gta ttt agc cat ctg 96
 Asn His Asn Tyr Leu Asn Ser Leu Pro Pro Gly Val Phe Ser His Leu
 20 25 30
 act gca tta agg gga cta agc ctc aac tcc aac agg ctg aca gtt ctt 144
 Thr Ala Leu Arg Gly Leu Ser Leu Asn Ser Asn Arg Leu Thr Val Leu
 35 40 45
 tct cac aat gat tta cct gct aat tta gag atc ctg gac ata tcc agg 192
 Ser His Asn Asp Leu Pro Ala Asn Leu Glu Ile Leu Asp Ile Ser Arg
 50 55 60
 aac cag ctc cta gct cct aat cct gat gta ttt gta tca ctt agt gtc 240
 Asn Gln Leu Leu Ala Pro Asn Pro Asp Val Phe Val Ser Leu Ser Val
 65 70 75 80
 ttg gat ata act cat aac aag ttc att tgt gaa tgt gaa ctt agc act 288
 Leu Asp Ile Thr His Asn Lys Phe Ile Cys Glu Cys Glu Leu Ser Thr
 85 90 95
 ttt atc aat tgg ctt aat cac acc aat gtc act ata gct ggg cct cct 336
 Phe Ile Asn Trp Leu Asn His Thr Asn Val Thr Ile Ala Gly Pro Pro
 100 105 110

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Ala	Asp	Ile	Tyr	Cys	Val	Tyr	Pro	Asp	Ser	Phe	Ser	Gly	Val	Ser	Leu	
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ttc	tct	ctt	tcc	acg	gaa	ggg	tgt	gat	gaa	gag	gaa	gtc	tta	aag	tcc	432
Phe	Ser	Leu	Ser	Thr	Glu	Gly	Cys	Asp	Glu	Glu	Glu	Val	Leu	Lys	Ser	
	130					135						140				
cta	aag	ttc	tcc	ctt	ttc	att	gta	tgc	act	gtc	act	ctg	act	ctg	ttc	480
Leu	Lys	Phe	Ser	Leu	Phe	Ile	Val	Cys	Thr	Val	Thr	Leu	Thr	Leu	Phe	
145					150					155					160	
ctc	atg	acc	atc	ctc	aca	gtc	aca	aag	ttc	cgg	ggc	ttc	tgt	ttt	atc	528
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Cys	Tyr	Lys	Thr	Ala	Gln	Arg	Leu	Val	Phe	Lys	Asp	His	Pro	Gln	Gly	
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Thr	Glu	Pro	Asp	Met	Tyr	Lys	Tyr	Asp	Ala	Tyr	Leu	Cys	Phe	Ser	Ser	
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Phe	Val	Pro	Gly	Glu	Asn	Arg	Ile	Ala	Asn	Ile	Gln	Asp	Ala	Ile	Trp	
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Asn	Ser	Arg	Lys	Ile	Val	Cys	Leu	Val	Ser	Arg	His	Phe	Leu	Arg	Asp	
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Gly	Trp	Cys	Leu	Glu	Ala	Phe	Ser	Tyr	Ala	Gln	Gly	Arg	Cys	Leu	Ser	
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Asp	Leu	Asn	Ser	Ala	Leu	Ile	Met	Val	Val	Val	Gly	Ser	Leu	Ser	Gln	
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Tyr	Gln	Leu	Met	Lys	His	Gln	Ser	Ile	Arg	Gly	Phe	Val	Gln	Lys	Gln	
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cag	tat	ttg	agg	tgg	cct	gag	gat	ctc	cag	gat	gtt	ggc	tgg	ttt	ctt	1008
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325

330

335

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Thr Ala Leu Arg Gly Leu Ser Leu Asn Ser Asn Arg Leu Thr Val Leu
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Ser His Asn Asp Leu Pro Ala Asn Leu Glu Ile Leu Asp Ile Ser Arg
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Asn Gln Leu Leu Ala Pro Asn Pro Asp Val Phe Val Ser Leu Ser Val
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Leu Asp Ile Thr His Asn Lys Phe Ile Cys Glu Cys Glu Leu Ser Thr
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Phe Ile Asn Trp Leu Asn His Thr Asn Val Thr Ile Ala Gly Pro Pro
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Ala Asp Ile Tyr Cys Val Tyr Pro Asp Ser Phe Ser Gly Val Ser Leu
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Phe Ser Leu Ser Thr Glu Gly Cys Asp Glu Glu Glu Val Leu Lys Ser
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Leu Lys Phe Ser Leu Phe Ile Val Cys Thr Val Thr Leu Thr Leu Phe
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Leu Met Thr Ile Leu Thr Val Thr Lys Phe Arg Gly Phe Cys Phe Ile
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 Cys Tyr Lys Thr Ala Gln Arg Leu Val Phe Lys Asp His Pro Gln Gly
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 Lys Asp Phe Thr Trp Val Gln Asn Ala Leu Leu Lys His Leu Asp Thr
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 Gln Tyr Ser Asp Gln Asn Arg Phe Asn Leu Cys Phe Glu Glu Arg Asp
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 Phe Val Pro Gly Glu Asn Arg Ile Ala Asn Ile Gln Asp Ala Ile Trp
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 Asn Ser Arg Lys Ile Val Cys Leu Val Ser Arg His Phe Leu Arg Asp
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 Gly Trp Cys Leu Glu Ala Phe Ser Tyr Ala Gln Gly Arg Cys Leu Ser
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 Asp Leu Asn Ser Ala Leu Ile Met Val Val Val Gly Ser Leu Ser Gln
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 Tyr Gln Leu Met Lys His Gln Ser Ile Arg Gly Phe Val Gln Lys Gln
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 Gln Tyr Leu Arg Trp Pro Glu Asp Leu Gln Asp Val Gly Trp Phe Leu
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Homo sapiens

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 Asp Val Thr Leu Asp Val Pro Lys Asn His Val Ile Val Asp Cys Thr
 15 20 25

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 Asp Lys His Leu Thr Glu Ile Pro Gly Gly Ile Pro Thr Asn Thr Thr
 30 35 40

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 Asn Leu Thr Leu Thr Ile Asn His Ile Pro Asp Ile Ser Pro Ala Ser
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 Phe His Arg Leu Asp His Leu Val Glu Ile Asp Phe Arg Cys Asn Cys
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 Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu
 75 80 85 90

cag att aaa ccc aga agc ttt agt gga ctc act tat tta aaa tcc ctt 384
 Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu
 95 100 105

tac ctg gat gga aac cag cta cta gag ata ccg cag ggc ctc ccg cct 432
 Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro
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 Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly
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 155 160 165 170

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Asp	Asn	Asn	Val	Thr	Ala	Val	Pro	Thr	Val	Leu	Pro	Ser	Thr	Leu	Thr	
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Glu	Leu	Tyr	Leu	Tyr	Asn	Asn	Met	Ile	Ala	Lys	Ile	Gln	Glu	Asp	Asp	
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Phe	Asn	Asn	Leu	Asn	Gln	Leu	Gln	Ile	Leu	Asp	Leu	Ser	Gly	Asn	Cys	
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Pro	Arg	Cys	Tyr	Asn	Ala	Pro	Phe	Pro	Cys	Ala	Pro	Cys	Lys	Asn	Asn	
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Ser	Pro	Leu	Gln	Ile	Pro	Val	Asn	Ala	Phe	Asp	Ala	Leu	Thr	Glu	Leu	
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Lys	Val	Leu	Arg	Leu	His	Ser	Asn	Ser	Leu	Gln	His	Val	Pro	Pro	Arg	
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Phe	Leu	Ala	Lys	Glu	Ile	Gly	Asp	Ala	Lys	Phe	Leu	His	Phe	Leu	Pro	
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Ser	Leu	Ile	Gln	Leu	Asp	Leu	Ser	Phe	Asn	Phe	Glu	Leu	Gln	Val	Tyr	
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Arg	Ala	Ser	Met	Asn	Leu	Ser	Gln	Ala	Phe	Ser	Ser	Leu	Lys	Ser	Leu	
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Lys	Ile	Leu	Arg	Ile	Arg	Gly	Tyr	Val	Phe	Lys	Glu	Leu	Lys	Ser	Phe	
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Asn	Leu	Ser	Pro	Leu	His	Asn	Leu	Gln	Asn	Leu	Glu	Val	Leu	Asp	Leu	
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Gly	Thr	Asn	Phe	Ile	Lys	Ile	Ala	Asn	Leu	Ser	Met	Phe	Lys	Gln	Phe	
	380					385					390					

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Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro Ser	
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Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr Ser Val	
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Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr Phe Arg Tyr	
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Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys Glu Ala Ser Phe	
445 450 455	
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Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly Gln Thr Leu Asp Leu	
460 465 470	
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Ser Lys Asn Ser Ile Phe Phe Val Lys Ser Ser Asp Phe Gln His Leu	
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Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn Leu Ile Ser Gln Thr	
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Phe Ser Asn Asn Arg Leu Asp Leu Leu His Ser Thr Ala Phe Glu Glu	
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Leu His Lys Leu Glu Val Leu Asp Ile Ser Ser Asn Ser His Tyr Phe	
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Gln Ser Glu Gly Ile Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys	
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Tyr	Phe	Leu	Gln	Asp	Ala	Phe	Gln	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	Ser	
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Cys	Asp	Ala	Val	Trp	Phe	Val	Trp	Trp	Val	Asn	His	Thr	Glu	Val	Thr	
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Ile	Pro	Tyr	Leu	Ala	Thr	Asp	Val	Thr	Cys	Val	Gly	Pro	Gly	Ala	His	
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815

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Ser Pro Leu Gln Ile Pro Val Asn Ala Phe Asp Ala Leu Thr Glu Leu 255 260 265		
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Arg Ala Ser Met Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu 335 340 345		
Lys Ile Leu Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe 350 355 360		
Asn Leu Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu 365 370 375		
Gly Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe 380 385 390		
Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro Ser 395 400 405 410		
Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr Ser Val 415 420 425		
Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr Phe Arg Tyr 430 435 440		
Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys Glu Ala Ser Phe 445 450 455		
Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly Gln Thr Leu Asp Leu 460 465 470		
Ser Lys Asn Ser Ile Phe Phe Val Lys Ser Ser Asp Phe Gln His Leu 475 480 485 490		
Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn Leu Ile Ser Gln Thr 495 500 505		

Leu Asn Gly Ser Glu Phe Gln Pro Leu Ala Glu Leu Arg Tyr Leu Asp
 510 515 520

Phe Ser Asn Asn Arg Leu Asp Leu Leu His Ser Thr Ala Phe Glu Glu
 525 530 535

Leu His Lys Leu Glu Val Leu Asp Ile Ser Ser Asn Ser His Tyr Phe
 540 545 550

Gln Ser Glu Gly Ile Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys
 555 560 565 570

Val Leu Gln Lys Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr
 575 580 585

Ser Arg Thr Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly
 590 595 600

Asn His Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln
 605 610 615

Leu Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn
 620 625 630

Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro Asn
 635 640 645 650

Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe Ser Trp
 655 660 665

Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp Leu Ser His
 670 675 680

Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn Cys Ser Arg Ser
 685 690 695

Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile Arg Ser Leu Thr Lys
 700 705 710

Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg Tyr Leu Asp Leu Ser Ser
 715 720 725 730

Asn Lys Ile Gln Met Ile Gln Lys Thr Ser Phe Pro Glu Asn Val Leu
 735 740 745

Asn Asn Leu Lys Met Leu Leu Leu His His Asn Arg Phe Leu Cys Thr
 750 755 760

Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn His Thr Glu Val Thr
 765 770 775

Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val Gly Pro Gly Ala His
 780 785 790

Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp
 795 800 805 810
 Leu Thr Asn Leu Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe
 815 820 825
 Leu Met Val Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp
 830 835 840
 Tyr Ile Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu
 845 850 855
 Ile Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys
 860 865 870
 Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys Leu
 875 880 885 890
 Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu Arg Asp
 895 900 905
 Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln Ser Ile Gln
 910 915 920
 Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys Tyr Ala Lys Thr
 925 930 935
 Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His Gln Arg Leu Met Asp
 940 945 950
 Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu Glu Lys Pro Phe Gln
 955 960 965 970
 Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu Cys Gly Ser Ser Val
 975 980 985
 Leu Glu Trp Pro Thr Asn Pro Gln Ala His Pro Tyr Phe Trp Gln Cys
 990 995 1000
 Leu Lys Asn Ala Leu Ala Thr Asp Asn His Val Ala Tyr Ser Gln Val
 1005 1010 1015
 Phe Lys Glu Thr Val
 1020

<210> 13

<211> 180

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:rodent; surmised

Mus musculus

<220>

<221> CDS

<222> (1)..(177)

<400> 13

ctt	gga	aaa	cct	ctt	cag	aag	tct	aag	ttt	ctt	cag	ctc	agg	aag	aga	48
Leu	Gly	Lys	Pro	Leu	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	Arg	
1				5					10					15		

ctc	tgc	agg	agc	tct	gtc	ctt	gag	tgg	cct	gca	aat	cca	cag	gct	cac	96
Leu	Cys	Arg	Ser	Ser	Val	Leu	Glu	Trp	Pro	Ala	Asn	Pro	Gln	Ala	His	
			20					25					30			

cca	tac	ttc	tgg	cag	tgc	ctg	aaa	aat	gcc	ctg	acc	aca	gac	aat	cat	144
Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Thr	Thr	Asp	Asn	His	
		35					40					45				

gtg	gct	tat	agt	caa	atg	ttc	aag	gaa	aca	gtc	tag					180
Val	Ala	Tyr	Ser	Gln	Met	Phe	Lys	Glu	Thr	Val						
	50					55										

<210> 14

<211> 59

<212> PRT

<213> Unknown

<400> 14

Leu	Gly	Lys	Pro	Leu	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	Arg	
1				5					10					15		

Leu	Cys	Arg	Ser	Ser	Val	Leu	Glu	Trp	Pro	Ala	Asn	Pro	Gln	Ala	His	
			20					25					30			

Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Thr	Thr	Asp	Asn	His	
		35				40						45				

Val	Ala	Tyr	Ser	Gln	Met	Phe	Lys	Glu	Thr	Val						
	50					55										

<210> 15

<211> 990

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>

<221> CDS

<222> (2) .. (988)

<400> 15

g aat tcc aga ctt ata aac ttg aaa aat ctc tat ttg gcc tgg aac tgc 49
Asn Ser Arg Leu Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn Cys
1 5 10 15

tat ttt aac aaa gtt tgc gag aaa act aac ata gaa gat gga gta ttt 97
Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile Glu Asp Gly Val Phe
20 25 30

gaa acg ctg aca aat ttg gag ttg cta tca cta tct ttc aat tct ctt 145
Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu
35 40 45

tca cat gtg cca ccc aaa ctg cca agc tcc cta cgc aaa ctt ttt ctg 193
Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu
50 55 60

agc aac acc cag atc aaa tac att agt gaa gaa gat ttc aag gga ttg 241
Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu Asp Phe Lys Gly Leu
65 70 75 80

atg aat tta aca tta cta gat tta agc ggg aac tgt ccg agg tgc ttc 289
Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly Asn Cys Pro Arg Cys Phe
85 90 95

aat gcc cca ttt cca tgc gtg cct tgt gat ggt ggt gct tca att aat 337
Asn Ala Pro Phe Pro Cys Val Pro Cys Asp Gly Gly Ala Ser Ile Asn
100 105 110

ata gat cgt ttt gct ttt caa aac ttg acc caa ctt cga tac cta aac 385
Ile Asp Arg Phe Ala Phe Gln Asn Leu Thr Gln Leu Arg Tyr Leu Asn
115 120 125

ctc tct agc act tcc ctc agg aag att aat gct gcc tgg ttt aaa aat 433
Leu Ser Ser Thr Ser Leu Arg Lys Ile Asn Ala Ala Trp Phe Lys Asn
130 135 140

atg cct cat ctg aag gtg ctg gat ctt gaa ttc aac tat tta gtg gga 481
Met Pro His Leu Lys Val Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly
145 150 155 160

gaa ata gcc tct ggg gca ttt tta acg atg ctg ccc cgc tta gaa ata 529
Glu Ile Ala Ser Gly Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile
165 170 175

ctt gac ttg tct ttt aac tat ata aag ggg agt tat cca cag cat att 577
Leu Asp Leu Ser Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile
180 185 190

aat att tcc aga aac ttc tct aaa ctt ttg tct cta cgg gca ttg cat 625
Asn Ile Ser Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His

195

200

205

tta aga ggt tat gtg ttc cag gaa ctc aga gaa gat gat ttc cag ccc 673
 Leu Arg Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro
 210 215 220

ctg atg cag ctt cca aac tta tcg act atc aac ttg ggt att aat ttt 721
 Leu Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe
 225 230 235 240

att aag caa atc gat ttc aaa ctt ttc caa aat ttc tcc aat ctg gaa 769
 Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu Glu
 245 250 255

att att tac ttg tca gaa aac aga ata tca ccg ttg gta aaa gat acc 817
 Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys Asp Thr
 260 265 270

cgg cag agt tat gca aat agt tcc tct ttt caa cgt cat atc cgg aaa 865
 Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His Ile Arg Lys
 275 280 285

cgg cgc tca aca gat ttt gag ttt gac cca cat tcg aac ttt tat cat 913
 Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser Asn Phe Tyr His
 290 295 300

ttc acc cgt cct tta ata aag cca caa tgt gct gct tat gga aaa gcc 961
 Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala Ala Tyr Gly Lys Ala
 305 310 315 320

tta gat tta agc ctc aac agt att ttc tt 990
 Leu Asp Leu Ser Leu Asn Ser Ile Phe
 325

<210> 16

<211> 329

<212> PRT

<213> Unknown

<400> 16

Asn Ser Arg Leu Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn Cys
 1 5 10 15

Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile Glu Asp Gly Val Phe
 20 25 30

Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu
 35 40 45

Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu
 50 55 60

Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu Asp Phe Lys Gly Leu

65	70	75	80
Ile Asn Leu Thr	Leu 85	Leu Asp Leu Ser Gly 90	Asn Cys Pro Arg Cys 95 Phe
Asn Ala Pro Phe	Pro 100	Cys Val Pro Cys Asp Gly Gly Ala Ser 110	Ile Asn
Ile Asp Arg	Phe 115	Ala Phe Gln Asn Leu Thr Gln Leu Arg Tyr 125	Leu Asn
Leu Ser Ser Thr	Ser 130	Leu Arg Lys Ile Asn Ala Ala Trp Phe Lys Asn 140	
Met Pro His Leu	Lys 145	Val Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly 160	
Glu Ile Ala Ser	Gly 165	Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile 175	
Leu Asp Leu Ser	Phe 180	Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile 190	
Asn Ile Ser Arg	Asn 195	Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His 205	
Leu Arg Gly Tyr	Val 210	Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro 220	
Leu Met Gln Leu	Pro 225	Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe 240	
Ile Lys Gln Ile	Asp 245	Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu Glu 255	
Ile Ile Tyr Leu	Ser 260	Glu Asn Arg Ile Ser Pro Leu Val Lys Asp Thr 270	
Arg Gln Ser Tyr	Ala 275	Asn Ser Ser Ser Phe Gln Arg His Ile Arg Lys 285	
Arg Arg Ser Thr	Asp 290	Phe Glu Phe Asp Pro His Ser Asn Phe Tyr His 300	
Phe Thr Arg Pro	Leu 305	Ile Lys Pro Gln Cys Ala Ala Tyr Gly Lys Ala 320	
Leu Asp Leu Ser	Leu 325	Asn Ser Ile Phe	

<210> 17
 <211> 1557

<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>
<221> CDS
<222> (1)..(513)

<220>
<221> misc_feature
<222> (93)..(149)
<223> Xaa translation depends on genetic code

<400> 17
cag tct ctt tcc aca tcc caa act ttc tat gat gct tac att tct tat 48
Gln Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr
1 5 10 15
gac acc aaa gat gcc tct gtt act gac tgg gtg ata aat gag ctg cgc 96
Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg
20 25 30
tac cac ctt gaa gag agc cga gac aaa aac gtt ctc ctt tgt cta gag 144
Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu
35 40 45
gag agg gat tgg gac ccg gga ttg gcc atc atc gac aac ctc atg cag 192
Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln
50 55 60
agc atc aac caa agc aag aaa aca gta ttt gtt tta acc aaa aaa tat 240
Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr
65 70 75 80
gca aaa agc tgg aac ttt aaa aca gct ttt tac ttg gsc ttg cag agg 288
Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Xaa Leu Gln Arg
85 90 95
cta atg ggt gag aac atg gat gtg att ata ttt atc ctg ctg gag cca 336
Leu Met Gly Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro
100 105 110
gtg tta cag cat tct ccg tat ttg agg cta cgg cag cgg atc tgt aag 384
Val Leu Gln His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys
115 120 125
agc tcc atc ctc cag tgg cct gac aac ccg aag gca gaa agg ttg ttt 432
Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Arg Leu Phe
130 135 140
tgg caa act ctg wga aat gtg gtc ttg act gaa aat gat tca cgg tat 480

Trp Gln Thr Leu Xaa Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr
 145 150 155 160

aac aat atg tat gtc gat tcc att aag caa tac taactgacgt taagtcatga 533
 Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr
 165 170

tttcgcgcca taataaagat gcaaaggaat gacatttcng tattagttat ctattgctan 593
 ggtaacnaaa ttantcccaa aaancttang tnggtttnaa aacaacnaca ttntgctggn 653
 cccacagttt ttgaggggtca ggagtcacagg cccagcataa ctgggtcttc tgcttcaggg 713
 tgtctncaga ggctgcaatg taggtgttca ccagagacat aggcactcact ggggtcacac 773
 tncatgtggt tgttttctgg attcaattcc tcttgggcta ttggccaaag gctataactca 833
 tgtaagccat gcgagcctat cccacaangg cagcttgctt catcagagct agcaaaaaag 893
 agaggttgct agcaagatga agtcacaatc ttttgaatc gaatcaaaaa agtgatatct 953
 catcactttg gccatattct atttggtaga agtaaaccac aggtcccacc agtccatgg 1013
 ggtgaccac ctcagtccag ggaaaacagc tgaagaccaa gatggtgagc tctgattgct 1073
 tcagttgggtc atcaactatt ttcccttgac tgctgtcctg ggatggccgg ctatcttgat 1133
 ggatagattg tgaatatcag gaggccaggg atcactgtgg accatcttag cagttgacct 1193
 aacacatctt cttttcaata tctaagaact tttgccactg tgactaatgg tctaataatt 1253
 aagctgttgt ttatatattat catatatcta tggctacatg gttatattat gctgtgggtg 1313
 ggttcgggtt tattttacagt tgcttttaca aatatttgct gtaacatttg acttctaagg 1373
 ttttagatgcc atttaagaac tgagatggat agctttttaa gcacttttta cttcttacca 1433
 ttttttaaaa gtatgcagct aaattcgaag cttttggtct atattgttaa ttgccattgc 1493
 tgtaaattctt aaaatgaatg aataaaaatg tttcatttta aaaaaaaaaa aaaaaaaaaa 1553
 aaaa 1557

<210> 18
 <211> 171
 <212> PRT
 <213> Unknown

<400> 18
 Gln Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr
 1 5 10 15

Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg
 20 25 30
 Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu
 35 40 45
 Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln
 50 55 60
 Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr
 65 70 75 80
 Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Xaa Leu Gln Arg
 85 90 95
 Leu Met Gly Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro
 100 105 110
 Val Leu Gln His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys
 115 120 125
 Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Arg Leu Phe
 130 135 140
 Trp Gln Thr Leu Xaa Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr
 145 150 155 160
 Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr
 165 170

<210> 19
 <211> 629
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:primate; surmised
 Homo sapiens

<220>
 <221> CDS
 <222> (1)..(486)

<220>
 <221> misc_feature
 <222> (48)..(75)
 <223> Xaa translation depends on genetic code

<400> 19
 aat gaa ttg atc ccc aat cta gag aag gaa gat ggt tct atc ttg att 48
 Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp Gly Ser Ile Leu Ile
 1 5 10 15

tgc ctt tat gaa agc tac ttt gac cct ggc aaa agc att agt gaa aat	96
Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly Lys Ser Ile Ser Glu Asn	
20 25 30	
att gta agc ttc att gag aaa agc tat aag tcc atc ttt gtt ttg tcy	144
Ile Val Ser Phe Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Xaa	
35 40 45	
ccc aac ttt gtc cag aat gag tgg tgc cat tat gaa ttc tac ttt gcc	192
Pro Asn Phe Val Gln Asn Glu Trp Cys His Tyr Glu Phe Tyr Phe Ala	
50 55 60	
cac cac aat ctc ttc cat gaa aat tct gat cay ata att ctt atc tta	240
His His Asn Leu Phe His Glu Asn Ser Asp Xaa Ile Ile Leu Ile Leu	
65 70 75 80	
ctg gaa ccc att cca ttc tat tgc att ccc acc agg tat cat aaa ctg	288
Leu Glu Pro Ile Pro Phe Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu	
85 90 95	
gaa gct ctc ctg gaa aaa aaa gca tac ttg gaa tgg ccc aag gat agg	336
Glu Ala Leu Leu Glu Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg	
100 105 110	
cgt aaa tgt ggg ctt ttc tgg gca aac ctt cga gct gct gtt aat gtt	384
Arg Lys Cys Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Val Asn Val	
115 120 125	
aat gta tta gcc acc aga gaa atg tat gaa ctg cag aca ttc aca gag	432
Asn Val Leu Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu	
130 135 140	
tta aat gaa gag tct cga ggt tct aca atc tct ctg atg aga aca gac	480
Leu Asn Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp	
145 150 155 160	
tgt cta taaaatccca cagtccttgg gaagttgggg accacataca ctgttgggat	536
Cys Leu	
gtacattgat acaaccttta tgatggcaat ttgacaatat ttattaaaat aaaaaatggt	596
tattcccttc aaaaaaaaaa aaaaaaaaaa aaa	629

<210> 20
 <211> 162
 <212> PRT
 <213> Unknown

<400> 20
 Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp Gly Ser Ile Leu Ile
 1 5 10 15

Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly Lys Ser Ile Ser Glu Asn
 20 25 30
 Ile Val Ser Phe Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Xaa
 35 40 45
 Pro Asn Phe Val Gln Asn Glu Trp Cys His Tyr Glu Phe Tyr Phe Ala
 50 55 60
 His His Asn Leu Phe His Glu Asn Ser Asp Xaa Ile Ile Leu Ile Leu
 65 70 75 80
 Leu Glu Pro Ile Pro Phe Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu
 85 90 95
 Glu Ala Leu Leu Glu Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg
 100 105 110
 Arg Lys Cys Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Val Asn Val
 115 120 125
 Asn Val Leu Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu
 130 135 140
 Leu Asn Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp
 145 150 155 160
 Cys Leu

<210> 21

<211> 427

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>

<221> CDS

<222> (1)..(426)

<400> 21

aag aac tcc aaa gaa aac ctc cag ttt cat gct ttt att tca tat agt 48
 Lys Asn Ser Lys Glu Asn Leu Gln Phe His Ala Phe Ile Ser Tyr Ser
 1 5 10 15

gaa cat gat tct gcc tgg gtg aaa agt gaa ttg gta cct tac cta gaa 96
 Glu His Asp Ser Ala Trp Val Lys Ser Glu Leu Val Pro Tyr Leu Glu
 20 25 30

aaa gaa gat ata cag att tgt ctt cat gag aga aac ttt gtc cct ggc 144

Lys Glu Asp Ile Gln Ile Cys Leu His Glu Arg Asn Phe Val Pro Gly
 35 40 45

aag agc att gtg gaa aat atc atc aac tgc att gag aag agt tac aag 192
 Lys Ser Ile Val Glu Asn Ile Ile Asn Cys Ile Glu Lys Ser Tyr Lys
 50 55 60

tcc atc ttt gtt ttg tct ccc aac ttt gtc cag agt gag tgg tgc cat 240
 Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Ser Glu Trp Cys His
 65 70 75 80

tac gaa ctc tat ttt gcc cat cac aat ctc ttt cat gaa gga tct aat 288
 Tyr Glu Leu Tyr Phe Ala His His Asn Leu Phe His Glu Gly Ser Asn
 85 90 95

aac tta atc ctc atc tta ctg gaa ccc att cca cag aac agc att ccc 336
 Asn Leu Ile Leu Ile Leu Leu Glu Pro Ile Pro Gln Asn Ser Ile Pro
 100 105 110

aac aag tac cac aag ctg aag gct ctc atg acg cag cgg act tat ttg 384
 Asn Lys Tyr His Lys Leu Lys Ala Leu Met Thr Gln Arg Thr Tyr Leu
 115 120 125

cag tgg ccc aag gag aaa agc aaa cgt ggg ctc ttt tgg gct a 427
 Gln Trp Pro Lys Glu Lys Ser Lys Arg Gly Leu Phe Trp Ala
 130 135 140

<210> 22

<211> 142

<212> PRT

<213> Unknown

<400> 22

Lys Asn Ser Lys Glu Asn Leu Gln Phe His Ala Phe Ile Ser Tyr Ser
 1 5 10 15

Glu His Asp Ser Ala Trp Val Lys Ser Glu Leu Val Pro Tyr Leu Glu
 20 25 30

Lys Glu Asp Ile Gln Ile Cys Leu His Glu Arg Asn Phe Val Pro Gly
 35 40 45

Lys Ser Ile Val Glu Asn Ile Ile Asn Cys Ile Glu Lys Ser Tyr Lys
 50 55 60

Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Ser Glu Trp Cys His
 65 70 75 80

Tyr Glu Leu Tyr Phe Ala His His Asn Leu Phe His Glu Gly Ser Asn
 85 90 95

Asn Leu Ile Leu Ile Leu Leu Glu Pro Ile Pro Gln Asn Ser Ile Pro

	100		105		110
Asn Lys Tyr His Lys Leu Lys Ala Leu Met Thr Gln Arg Thr Tyr Leu					
	115		120		125
Gln Trp Pro Lys Glu Lys Ser Lys Arg Gly Leu Phe Trp Ala					
	130		135		140

<210> 23
 <211> 662
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:primate; surmised
 Homo sapiens

<220>
 <221> CDS
 <222> (1)..(627)
 <220>
 <221> misc_feature
 <222> (18)..(136)
 <223> Xaa translation depends on genetic code

<400> 23	
gct tcc acc tgt gcc tgg cct ggc ttc cct ggc ggg ggc ggc aaa gtg	48
Ala Ser Thr Cys Ala Trp Pro Gly Phe Pro Gly Gly Gly Gly Lys Val	
	5 10 15
ggc gar atg agg atg ccc tgc cct acg atg cct tcg tgg tct tcg aca	96
Gly Xaa Met Arg Met Pro Cys Pro Thr Met Pro Ser Trp Ser Ser Thr	
	20 25 30
aaa cgc rga gcg cag tgg cag act ggg tgt aca acg agc ttc ggg ggc	144
Lys Arg Xaa Ala Gln Trp Gln Thr Gly Cys Thr Thr Ser Phe Gly Gly	
	35 40 45
agc tgg agg agt gcc gtg ggc gct ggg cac tcc gcc tgt gcc tgg agg	192
Ser Trp Arg Ser Ala Val Gly Ala Gly His Ser Ala Cys Ala Trp Arg	
	50 55 60
aac gcg act ggc tgc ctg gca aaa ccc tct ttg aga acc tgt ggg cct	240
Asn Ala Thr Gly Cys Leu Ala Lys Pro Ser Leu Arg Thr Cys Gly Pro	
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cgg tct atg gca gcc gca aga cgc tgt ttg tgc tgg ccc aca cgg acc	288
Arg Ser Met Ala Ala Ala Arg Arg Cys Leu Cys Trp Pro Thr Arg Thr	
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ggg tca gtg gtc tct tgc gcg cca ktt ntc ctg ctg gcc cag cag cgc	336
Gly Ser Val Val Ser Cys Ala Pro Xaa Xaa Leu Leu Ala Gln Gln Arg	

100										105					110					
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Leu	Leu	Xaa	Asp	Arg	Lys	Asp	Val	Val	Val	Leu	Val	Ile	Leu	Xaa	Pro					
		115					120					125								
gac	ggc	caa	gcc	tcc	cga	cta	cnn	gat	gcg	ctg	acc	agc	gcc	tct	gcc	432				
Asp	Gly	Gln	Ala	Ser	Arg	Leu	Xaa	Asp	Ala	Leu	Thr	Ser	Ala	Ser	Ala					
	130					135					140									
gcc	aga	gtg	tcc	tcc	tct	ggc	ccc	acc	agc	cca	gtg	gtc	gcg	cag	ctt	480				
Ala	Arg	Val	Ser	Ser	Ser	Gly	Pro	Thr	Ser	Pro	Val	Val	Ala	Gln	Leu					
145					150					155					160					
ctg	agg	cca	gca	tgc	atg	gcc	ctg	acc	agg	gac	aac	cac	cac	ttc	tat	528				
Leu	Arg	Pro	Ala	Cys	Met	Ala	Leu	Thr	Arg	Asp	Asn	His	His	Phe	Tyr					
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Asn	Arg	Asn	Phe	Cys	Gln	Gly	Thr	His	Gly	Arg	Ile	Ala	Val	Ser	Arg					
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Asn	Pro	Ala	Arg	Cys	His	Leu	His	Thr	His	Leu	Thr	Tyr	Ala	Cys	Leu					
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 Lys Arg Xaa Ala Gln Trp Gln Thr Gly Cys Thr Thr Ser Phe Gly Gly
 35 40 45
 Ser Trp Arg Ser Ala Val Gly Ala Gly His Ser Ala Cys Ala Trp Arg
 50 55 60
 Asn Ala Thr Gly Cys Leu Ala Lys Pro Ser Leu Arg Thr Cys Gly Pro
 65 70 75 80
 Arg Ser Met Ala Ala Ala Arg Arg Cys Leu Cys Trp Pro Thr Arg Thr
 85 90 95

cagggccact gctgctcaca naascagtga ggatgatgcc aggatg atg tct gcc 115
Met Ser Ala
-20

tcg cgc ctg gct ggg act ctg atc cca gcc atg gcc ttc ctc tcc tgc	163
Ser Arg Leu Ala Gly Thr Leu Ile Pro Ala Met Ala Phe Leu Ser Cys	
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gtg aga cca gaa agc tgg gag ccc tgc gtg gag gtt cct aat att act	211
Val Arg Pro Glu Ser Trp Glu Pro Cys Val Glu Val Pro Asn Ile Thr	
-1 1 5 10	
tat caa tgc atg gag ctg aat ttc tac aaa atc ccc gac aac ctc ccc	259
Tyr Gln Cys Met Glu Leu Asn Phe Tyr Lys Ile Pro Asp Asn Leu Pro	
15 20 25	
ttc tca acc aag aac ctg gac ctg agc ttt aat ccc ctg agg cat tta	307
Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe Asn Pro Leu Arg His Leu	
30 35 40 45	
ggc agc tat agc ttc ttc agt ttc cca gaa ctg cag gtg ctg gat tta	355
Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu Leu Gln Val Leu Asp Leu	
50 55 60	
tcc agg tgt gaa atc cag aca att gaa gat ggg gca tat cag agc cta	403
Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr Gln Ser Leu	
65 70 75	
agg cac ctc tct acc tta ata ttg aca gga aac ccc atc cag agt tta	451
Ser His Leu Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile Gln Ser Leu	
80 85 90	
ggc ctg gga gcc ttt tct gga cta tca agt tta cag aag ctg gtg gct	499
Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala	
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gtg gag aca aat cta gca tct cta gag aac ttc ccc att gga cat ctc	547
Val Glu Thr Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile Gly His Leu	
110 115 120 125	
aaa act ttg aaa gaa ctt aat gtg gct cac aat ctt atc caa tct ttc	595
Lys Thr Leu Lys Glu Leu Asn Val Ala His Asn Leu Ile Gln Ser Phe	
130 135 140	
aaa tta cct gag tat ttt tct aat ctg acc aat cta gag cac ttg gac	643
Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu His Leu Asp	
145 150 155	
ctt tcc agc aac aag att caa agt att tat tgc aca gac ttg cgg gtt	691
Leu Ser Ser Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp Leu Arg Val	
160 165 170	
cta cat caa atg ccc cta ctc aat ctc tct tta gac ctg tcc ctg aay	739
Leu His Gln Met Pro Leu Leu Asn Leu Ser Leu Asp Leu Ser Leu Xaa	
175 180 185	

cct atg aac ttt atc caa cca ggt gca ttt aaa gaa att agg ctt cat	787
Pro Met Asn Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu His	
190 195 200 205	
aag ctg act tta aga aat aat ttt gat agt tta aat gta atg aaa act	835
Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser Leu Asn Val Met Lys Thr	
210 215 220	
tgt att caa ggt ctg gct ggt tta gaa gtc cat cgt ttg gtt ctg gga	883
Cys Ile Gln Gly Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly	
225 230 235	
gaa ttt aga aat gaa gga aac ttg gaa aag ttt gac aaa tct gct cta	931
Glu Phe Arg Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys Ser Ala Leu	
240 245 250	
gag ggc ctg tgc aat ttg acc att gaa gaa ttc cga tta gca tac tta	979
Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu Ala Tyr Leu	
255 260 265	
gac tac tac ctc gat gat att att gac tta ttt aat tgt ttg aca aat	1027
Asp Tyr Tyr Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Thr Asn	
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Val Ser Ser Phe Ser Leu Val Ser Val Thr Ile Glu Arg Val Lys Asp	
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Phe Ser Tyr Asn Phe Gly Trp Gln His Leu Glu Leu Val Asn Cys Lys	
305 310 315	
ttt gga cag ttt ccc aca ttg aaa ctc aaa tct ctc aaa agg ctt act	1171
Phe Gly Gln Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr	
320 325 330	
ttc act tcc aac aaa ggt ggg aat gct ttt tca gaa gtt gat cta cca	1219
Phe Thr Ser Asn Lys Gly Gly Asn Ala Phe Ser Glu Val Asp Leu Pro	
335 340 345	
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Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser Phe Lys Gly	
350 355 360 365	
tgc tgt tct caa agt gat ttt ggg aca acc agc cta aag tat tta gat	1315
Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys Tyr Leu Asp	
370 375 380	
ctg agc ttc aat ggt gtt att acc atg agt tca aac ttc ttg ggc tta	1363
Leu Ser Phe Asn Gly Val Ile Thr Met Ser Ser Asn Phe Leu Gly Leu	
385 390 395	
gaa caa cta gaa cat ctg gat ttc cag cat tcc aat ttg aaa caa atg	1411
Glu Gln Leu Glu His Leu Asp Phe Gln His Ser Asn Leu Lys Gln Met	

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Ser	Glu	Phe	Ser	Val	Phe	Leu	Ser	Leu	Arg	Asn	Leu	Ile	Tyr	Leu	Asp					
415						420			425											
att	tct	cat	act	cac	acc	aga	gtt	gct	ttc	aat	ggc	atc	ttc	aat	ggc	1507				
Ile	Ser	His	Thr	His	Thr	Arg	Val	Ala	Phe	Asn	Gly	Ile	Phe	Asn	Gly					
430			435						440			445								
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aac	ttc	ctt	cca	gat	atc	ttc	aca	gag	ctg	aga	aac	ttg	acc	ttc	ctg	1603				
Asn	Phe	Leu	Pro	Asp	Ile	Phe	Thr	Glu	Leu	Arg	Asn	Leu	Thr	Phe	Leu					
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gac	ctc	tct	cag	tgt	caa	ctg	gag	cag	ttg	tct	cca	aca	gca	ttt	aac	1651				
Asp	Leu	Ser	Gln	Cys	Gln	Leu	Glu	Gln	Leu	Ser	Pro	Thr	Ala	Phe	Asn					
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tca	ctc	tcc	agt	ctt	cag	gta	cta	aat	atg	agc	cac	aac	aac	ttc	ttt	1699				
Ser	Leu	Ser	Ser	Leu	Gln	Val	Leu	Asn	Met	Ser	His	Asn	Asn	Phe	Phe					
495						500			505											
tca	ttg	gat	acg	ttt	cct	tat	aag	tgt	ctg	aac	tcc	ctc	cag	gtt	ctt	1747				
Ser	Leu	Asp	Thr	Phe	Pro	Tyr	Lys	Cys	Leu	Asn	Ser	Leu	Gln	Val	Leu					
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Asp	Tyr	Ser	Leu	Asn	His	Ile	Met	Thr	Ser	Lys	Lys	Gln	Glu	Leu	Gln					
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cat	ttt	cca	agt	agt	cta	gct	ttc	tta	aat	ctt	act	cag	aat	gac	ttt	1843				
His	Phe	Pro	Ser	Ser	Leu	Ala	Phe	Leu	Asn	Leu	Thr	Gln	Asn	Asp	Phe					
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gct	tgt	act	tgt	gaa	cac	cag	agt	ttc	ctg	caa	tgg	atc	aag	gac	cag	1891				
Ala	Cys	Thr	Cys	Glu	His	Gln	Ser	Phe	Leu	Gln	Trp	Ile	Lys	Asp	Gln					
560						565			570											
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575						580			585											
gat	aag	cag	ggc	atg	cct	gtg	ctg	agt	ttg	aat	atc	acc	tgt	cag	atg	1987				
Asp	Lys	Gln	Gly	Met	Pro	Val	Leu	Ser	Leu	Asn	Ile	Thr	Cys	Gln	Met					
590			595						600			605								
aat	aag	acc	atc	att	ggc	gtg	tgc	gtc	ctc	agt	gtg	ctt	gta	gta	tct	2035				
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gtt gta gca gtt ctg gtc tat aag ttc tat ttt cac ctg atg ctt ctt	2083
Val Val Ala Val Leu Val Tyr Lys Phe Tyr Phe His Leu Met Leu Leu	
625 630 635	
gct ggc tgc ata aag tat ggt aga ggt gaa aac atc tat gat gcc ttt	2131
Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu Asn Ile Tyr Asp Ala Phe	
640 645 650	
gtt atc tac tca agc cag gat gag gac tgg gta agg aat gag cta gta	2179
Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp Val Arg Asn Glu Leu Val	
655 660 665	
aag aat tta gaa gaa ggg gtg cct cca ttt cag ctc tgc ctt cac tac	2227
Lys Asn Leu Glu Glu Gly Val Pro Pro Phe Gln Leu Cys Leu His Tyr	
670 675 680 685	
aga gac ttt att ccc ggt gtg gcc att gct gcc aac atc atc cat gaa	2275
Arg Asp Phe Ile Pro Gly Val Ala Ile Ala Ala Asn Ile Ile His Glu	
690 695 700	
ggg ttc cat aaa agc cga aag gtg att gtt gtg gtg tcc cag cac ttc	2323
Gly Phe His Lys Ser Arg Lys Val Ile Val Val Val Ser Gln His Phe	
705 710 715	
atc cag agc cgc tgg tgt atc ttt gaa tat gag att gct cag acc tgg	2371
Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala Gln Thr Trp	
720 725 730	
cag ttt ctg agc agt cgt gct ggt atc atc ttc att gtc ctg cag aag	2419
Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile Phe Ile Val Leu Gln Lys	
735 740 745	
gtg gag aag acc ctg ctc agg cag cag gtg gag ctg tac cgc ctt ctc	2467
Val Glu Lys Thr Leu Leu Arg Gln Gln Val Glu Leu Tyr Arg Leu Leu	
750 755 760 765	
agc agg aac act tac ctg gag tgg gag gac agt gtc ctg ggg cgg cac	2515
Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu Gly Arg His	
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Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu Leu Asp Gly Lys Ser Trp	
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aat cca gaa gga aca gtg ggt aca gga tgc aat tgg cag gaa gca aca	2611
Asn Pro Glu Gly Thr Val Gly Thr Gly Cys Asn Trp Gln Glu Ala Thr	
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tct atc tgaagaggaa aaataaaaac ctctgaggc atttcttgcc cagctgggtc	2667
Ser Ile	
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 atctcacttc tgtatatata cccaaaataa ttgaaatcag aatttcaaga aatatttac 4227
 actcccatgt tcattgtggc actcttcaca atcactgttt ccaaagttat ggaacaacc 4287

Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His Asn Leu Ile
 125 130 135
 Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu
 140 145 150
 His Leu Asp Leu Ser Ser Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp
 155 160 165 170
 Leu Arg Val Leu His Gln Met Pro Leu Leu Asn Leu Ser Leu Asp Leu
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 Ser Leu Xaa Pro Met Asn Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile
 190 195 200
 Arg Leu His Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser Leu Asn Val
 205 210 215
 Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val His Arg Leu
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 Val Leu Gly Glu Phe Arg Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys
 235 240 245 250
 Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu
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 Ala Tyr Leu Asp Tyr Tyr Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys
 270 275 280
 Leu Thr Asn Val Ser Ser Phe Ser Leu Val Ser Val Thr Ile Glu Arg
 285 290 295
 Val Lys Asp Phe Ser Tyr Asn Phe Gly Trp Gln His Leu Glu Leu Val
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 Asn Cys Lys Phe Gly Gln Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys
 315 320 325 330
 Arg Leu Thr Phe Thr Ser Asn Lys Gly Gly Asn Ala Phe Ser Glu Val
 335 340 345
 Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser
 350 355 360
 Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys
 365 370 375
 Tyr Leu Asp Leu Ser Phe Asn Gly Val Ile Thr Met Ser Ser Asn Phe
 380 385 390
 Leu Gly Leu Glu Gln Leu Glu His Leu Asp Phe Gln His Ser Asn Leu
 395 400 405 410

Lys Gln Met Ser Glu Phe Ser Val Phe Leu Ser Leu Arg Asn Leu Ile
 415 420 425
 Tyr Leu Asp Ile Ser His Thr His Thr Arg Val Ala Phe Asn Gly Ile
 430 435 440
 Phe Asn Gly Leu Ser Ser Leu Glu Val Leu Lys Met Ala Gly Asn Ser
 445 450 455
 Phe Gln Glu Asn Phe Leu Pro Asp Ile Phe Thr Glu Leu Arg Asn Leu
 460 465 470
 Thr Phe Leu Asp Leu Ser Gln Cys Gln Leu Glu Gln Leu Ser Pro Thr
 475 480 485 490
 Ala Phe Asn Ser Leu Ser Ser Leu Gln Val Leu Asn Met Ser His Asn
 495 500 505
 Asn Phe Phe Ser Leu Asp Thr Phe Pro Tyr Lys Cys Leu Asn Ser Leu
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 Gln Val Leu Asp Tyr Ser Leu Asn His Ile Met Thr Ser Lys Lys Gln
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 Glu Leu Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn Leu Thr Gln
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 Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu Gln Trp Ile
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 Lys Asp Gln Arg Gln Leu Leu Val Glu Val Glu Arg Met Glu Cys Ala
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 Thr Pro Ser Asp Lys Gln Gly Met Pro Val Leu Ser Leu Asn Ile Thr
 590 595 600
 Cys Gln Met Asn Lys Thr Ile Ile Gly Val Ser Val Leu Ser Val Leu
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 Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr Phe His Leu
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 635 640 645 650
 Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp Val Arg Asn
 655 660 665
 Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe Gln Leu Cys
 670 675 680
 Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala Ala Asn Ile
 685 690 695

Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val Val Val Ser
700 705 710

Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala
715 720 725 730

Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile Phe Ile Val
735 740 745

Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Gln Gln Val Glu Leu Tyr
750 755 760

Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu
765 770 775

Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu Leu Asp Gly
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<212> DNA

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<223> Description of Unknown Organism:rodent; surmised
Mus musculus

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<222> (1)..(300)

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<223> Xaa translation depends on genetic code

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Val Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Thr Leu
20 25 30

cca cct aat tta cta gag ctc tat ctt tat aac aat atc att aag aaa	144
Pro Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys	
35 40 45	
atc caa gaa aat gat ttc aat aac ctc aat gag ttg caa gtn ctt gac	192
Ile Gln Glu Asn Asp Phe Asn Asn Leu Asn Glu Leu Gln Xaa Leu Asp	
50 55 60	
cta ngf gga aat tgc cct cga tgt nat aat gtc cca tat ccg tgt aca	240
Leu Xaa Gly Asn Cys Pro Arg Cys Xaa Asn Val Pro Tyr Pro Cys Thr	
65 70 75 80	
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Ser Ser Thr Xaa	
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Val Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Thr Leu	
20 25 30	
Pro Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys	
35 40 45	
Ile Gln Glu Asn Asp Phe Asn Asn Leu Asn Glu Leu Gln Xaa Leu Asp	
50 55 60	
Leu Xaa Gly Asn Cys Pro Arg Cys Xaa Asn Val Pro Tyr Pro Cys Thr	
65 70 75 80	
Pro Cys Glu Asn Asn Ser Pro Leu Gln Ile His Xaa Asn Ala Phe Asn	
85 90 95	
Ser Ser Thr Xaa	
100	

<210> 29
 <211> 1756
 <212> DNA
 <213> Unknown

<220>
<223> Description of Unknown Organism:rodent; surmised
Mus musculus

<220>
<221> CDS
<222> (1)..(1182)

<400> 29
tct cca gaa att ccc tgg aat tcc ttg cct cct gag gtt ttt gag ggt 48
Ser Pro Glu Ile Pro Trp Asn Ser Leu Pro Pro Glu Val Phe Glu Gly
1 5 10 15
atg ccg cca aat cta aag aat ctc tcc ttg gcc aaa aat ggg ctc aaa 96
Met Pro Pro Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys
20 25 30
tct ttc ttt tgg gac aga ctc cag tta ctg aag cat ttg gaa att ttg 144
Ser Phe Phe Trp Asp Arg Leu Gln Leu Leu Lys His Leu Glu Ile Leu
35 40 45
gac ctc agc cat aac cag ctg aca aaa gta cct gag aga ttg gcc aac 192
Asp Leu Ser His Asn Gln Leu Thr Lys Val Pro Glu Arg Leu Ala Asn
50 55 60
tgt tcc aaa agt ctc aca aca ctg att ctt aag cat aat caa atc agg 240
Cys Ser Lys Ser Leu Thr Thr Leu Ile Leu Lys His Asn Gln Ile Arg
65 70 75 80
caa ttg aca aaa tat ttt cta gaa gat gct ttg caa ttg cgc tat cta 288
Gln Leu Thr Lys Tyr Phe Leu Glu Asp Ala Leu Gln Leu Arg Tyr Leu
85 90 95
gac atc agt tca aat aaa atc cag gtc att cag aag act agc ttc cca 336
Asp Ile Ser Ser Asn Lys Ile Gln Val Ile Gln Lys Thr Ser Phe Pro
100 105 110
gaa aat gtc ctc aac aat ctg gag atg ttg gtt tta cat cac aat cgc 384
Glu Asn Val Leu Asn Asn Leu Glu Met Leu Val Leu His His Asn Arg
115 120 125
ttt ctt tgc aac tgt gat gct gtg tgg ttt gtc tgg tgg gtt aac cat 432
Phe Leu Cys Asn Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn His
130 135 140
aca gat gtt act att cca tac ctg gcc act gat gtg act tgt gta ggt 480
Thr Asp Val Thr Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val Gly
145 150 155 160
cca gga gca cac aaa ggt caa agt gtc ata tcc ctt gat ctg tat acg 528
Pro Gly Ala His Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr Thr
165 170 175

tgt gag tta gat ctc aca aac ctg att ctg ttc tca gtt tcc ata tca	576
Cys Glu Leu Asp Leu Thr Asn Leu Ile Leu Phe Ser Val Ser Ile Ser	
180 185 190	
tca gtc ctc ttt ctt atg gta gtt atg aca aca agt cac ctc ttt ttc	624
Ser Val Leu Phe Leu Met Val Val Met Thr Thr Ser His Leu Phe Phe	
195 200 205	
tgg gat atg tgg tac att tat tat ttt tgg aaa gca aag ata aag ggg	672
Trp Asp Met Trp Tyr Ile Tyr Tyr Phe Trp Lys Ala Lys Ile Lys Gly	
210 215 220	
tat cca gca tct gca atc cca tgg agt cct tgt tat gat gct ttt att	720
Tyr Pro Ala Ser Ala Ile Pro Trp Ser Pro Cys Tyr Asp Ala Phe Ile	
225 230 235 240	
gtg tat gac act aaa aac tca gct gtg aca gaa tgg gtt ttg cag gag	768
Val Tyr Asp Thr Lys Asn Ser Ala Val Thr Glu Trp Val Leu Gln Glu	
245 250 255	
ctg gtg gca aaa ttg gaa gat cca aga gaa aaa cac ttc aat ttg tgt	816
Leu Val Ala Lys Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys	
260 265 270	
cta gaa gaa aga gac tgg cta cca gga cag cca gtt cta gaa aac ctt	864
Leu Glu Glu Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu	
275 280 285	
tct cag agc ata cag ctc agc aaa aag aca gtg ttt gtg atg aca cag	912
Ser Gln Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Gln	
290 295 300	
aaa tat gct aag act gag agt ttt aag atg gca ttt tat ttg tct cat	960
Lys Tyr Ala Lys Thr Glu Ser Phe Lys Met Ala Phe Tyr Leu Ser His	
305 310 315 320	
cag agg ctc ctg gat gaa aaa gtg gat gtg att atc ttg ata ttc ttg	1008
Gln Arg Leu Leu Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu	
325 330 335	
gaa aga cct ctt cag aag tct aag ttt ctt cag ctc agg aag aga ctc	1056
Glu Arg Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu	
340 345 350	
tgc agg agc tct gtc ctt gag tgg cct gca aat cca cag gct cac cca	1104
Cys Arg Ser Ser Val Leu Glu Trp Pro Ala Asn Pro Gln Ala His Pro	
355 360 365	
tac ttc tgg cag tgc ctg aaa aat gcc ctg acc aca gac aat cat gtg	1152
Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn His Val	
370 375 380	
gct tat agt caa atg ttc aag gaa aca gtc tagctctctg aagaatgtca	1202
Ala Tyr Ser Gln Met Phe Lys Glu Thr Val	

385

390

ccacctagga catgccttgg tacctgaagt tttcataaag gtttccataa atgaaggtct 1262
 gaatttttcc taacagttgt catggctcag attggtggga aatcatcaat atatggctaa 1322
 gaaattaaga aggggagact gatagaagat aatttctttc ttcattgtgcc atgctcagtt 1382
 aaatatttcc cctagctcaa atctgaaaaa ctgtgcctag gagacaacac aaggctttga 1442
 tttatctgca tacaattgat aagagccaca catctgcctt gaagaagtac tagtagtttt 1502
 agtagtaggg taaaaattac acaagctttc tctctctctg atactgaact gtaccagagt 1562
 tcaatgaaat aaaagcccag agaacttctc agtaaattgg ttcattatca tgtagtatcc 1622
 accatgcaat atgccacaaa rccgctactg gtacaggaca gntggtagct gcttcaakgc 1682
 ctcttatcat tttcttgggg cccatggagg gggtctytgg gaaadaggga agkttttttt 1742
 1756
 tggccatcca tgaa

<210> 30

<211> 394

<212> PRT

<213> Unknown

<400> 30

Ser Pro Glu Ile Pro Trp Asn Ser Leu Pro Pro Glu Val Phe Glu Gly
 1 5 10 15

Met Pro Pro Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys
 20 25 30

Ser Phe Phe Trp Asp Arg Leu Gln Leu Leu Lys His Leu Glu Ile Leu
 35 40 45

Asp Leu Ser His Asn Gln Leu Thr Lys Val Pro Glu Arg Leu Ala Asn
 50 55 60

Cys Ser Lys Ser Leu Thr Thr Leu Ile Leu Lys His Asn Gln Ile Arg
 65 70 75 80

Gln Leu Thr Lys Tyr Phe Leu Glu Asp Ala Leu Gln Leu Arg Tyr Leu
 85 90 95

Asp Ile Ser Ser Asn Lys Ile Gln Val Ile Gln Lys Thr Ser Phe Pro
 100 105 110

Glu Asn Val Leu Asn Asn Leu Glu Met Leu Val Leu His His Asn Arg
 115 120 125

Phe Leu Cys Asn Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn His
 130 135 140
 Thr Asp Val Thr Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val Gly
 145 150 155 160
 Pro Gly Ala His Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr Thr
 165 170 175
 Cys Glu Leu Asp Leu Thr Asn Leu Ile Leu Phe Ser Val Ser Ile Ser
 180 185 190
 Ser Val Leu Phe Leu Met Val Val Met Thr Thr Ser His Leu Phe Phe
 195 200 205
 Trp Asp Met Trp Tyr Ile Tyr Tyr Phe Trp Lys Ala Lys Ile Lys Gly
 210 215 220
 Tyr Pro Ala Ser Ala Ile Pro Trp Ser Pro Cys Tyr Asp Ala Phe Ile
 225 230 235 240
 Val Tyr Asp Thr Lys Asn Ser Ala Val Thr Glu Trp Val Leu Gln Glu
 245 250 255
 Leu Val Ala Lys Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys
 260 265 270
 Leu Glu Glu Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu
 275 280 285
 Ser Gln Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Gln
 290 295 300
 Lys Tyr Ala Lys Thr Glu Ser Phe Lys Met Ala Phe Tyr Leu Ser His
 305 310 315 320
 Gln Arg Leu Leu Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu
 325 330 335
 Glu Arg Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu
 340 345 350
 Cys Arg Ser Ser Val Leu Glu Trp Pro Ala Asn Pro Gln Ala His Pro
 355 360 365
 Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn His Val
 370 375 380
 Ala Tyr Ser Gln Met Phe Lys Glu Thr Val
 385 390

<210> 31
 <211> 999

<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>
<221> CDS
<222> (2)..(847)

<220>
<221> misc_feature
<222> (1)..(282)
<223> Xaa translation depends on genetic code

<400> 31
c tcn gat gcc aag att cgg cac nag gca tat tca gag gtc atg atg gtt 49
Xaa Asp Ala Lys Ile Arg His Xaa Ala Tyr Ser Glu Val Met Met Val
1 5 10 15
ggg tgg tca gat tca tac acc tgt gaa tac cct tta aac cta agg gga 97
Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly
20 25 30
acc agg tta aaa gac gtt cat ctc cac gaa tta tct tgc aac aca gct 145
Thr Arg Leu Lys Asp Val His Leu His Glu Leu Ser Cys Asn Thr Ala
35 40 45
ctg ttg att gtc acc att gtg gtt att atg cta gtt ctg ggg ttg gct 193
Leu Leu Ile Val Thr Ile Val Val Ile Met Leu Val Leu Gly Leu Ala
50 55 60
gtg gcc ttc tgc tgt ctc cac ttt gat ctg ccc tgg tat ctc agg atg 241
Val Ala Phe Cys Cys Leu His Phe Asp Leu Pro Trp Tyr Leu Arg Met
65 70 75 80
cta ggt caa tgc aca caa aca tgg cac agg gtt agg aaa aca acc caa 289
Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr Gln
85 90 95
gaa caa ctc aag aga aat gtc cga ttc cac gca ttt att tca tac agt 337
Glu Gln Leu Lys Arg Asn Val Arg Phe His Ala Phe Ile Ser Tyr Ser
100 105 110
gaa cat gat tct ctg tgg gtg aag aat gaa ttg atc ccc aat cta gag 385
Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu Glu
115 120 125
aag gaa gat ggt tct atc ttg att tgc ctt tat gaa agc tac ttt gac 433
Lys Glu Asp Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe Asp
130 135 140

cct ggc aaa agc att agt gaa aat att gta agc ttc att gag aaa agc 481
Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys Ser 160
145 150 155

tat aag tcc atc ttt gtt ttg tct ccc aac ttt gtc cag aat gag tgg 529
Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu Trp 175
165 170

tgc cat tat gaa ttc tac ttt gcc cac cac aat ctc ttc cat gaa aat 577
Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu Asn 190
180 185

tct gat cac ata att ctt atc tta ctg gaa ccc att cca ttc tat tgc 625
Ser Asp His Ile Ile Leu Ile Leu Leu Glu Pro Ile Pro Phe Tyr Cys 205
195 200

att ccc acc agg tat cat aaa ctg raa gct ctc ctg gaa aaa aaa gca 673
Ile Pro Thr Arg Tyr His Lys Leu Xaa Ala Leu Leu Glu Lys Lys Ala 220
210 215

tac ttg gaa tgg ccc aag gat agg cgt aaa tgt ggg ctt tty tgg gca 721
Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Xaa Trp Ala 240
225 230 235

aac ctt cga gct gct gtt aat gtt aat gta tta gcc acc aga gaa atg 769
Asn Leu Arg Ala Ala Val Asn Val Asn Val Leu Ala Thr Arg Glu Met 255
245 250

tat gaa ctg cag aca ttc aca gag tta aat gaa gag tct cga ggt tct 817
Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly Ser 270
260 265

aca atc tyt ctg atg aga aca gac tgt yta taaaatccca cagtccttgg 867
Thr Ile Xaa Leu Met Arg Thr Asp Cys Xaa 280
275

gaagttgggg accacataca ctgttgggat gtacattgat acaaccttta tgatggcaat 927
ttgacaatat ttattaaaat aaaaaatggt tattcccttc aaaaaaaaaa aaaaaaaaaa 987
aaaaaaaaaa aa 999

<210> 32
<211> 282
<212> PRT
<213> Unknown

<400> 32
Xaa Asp Ala Lys Ile Arg His Xaa Ala Tyr Ser Glu Val Met Met Val
1 5 10 15

Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly
20 25 30

Thr Arg Leu Lys Asp Val His Leu His Glu Leu Ser Cys Asn Thr Ala
 35 40 45
 Leu Leu Ile Val Thr Ile Val Val Ile Met Leu Val Leu Gly Leu Ala
 50 55 60
 Val Ala Phe Cys Cys Leu His Phe Asp Leu Pro Trp Tyr Leu Arg Met
 65 70 75 80
 Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr Gln
 85 90 95
 Glu Gln Leu Lys Arg Asn Val Arg Phe His Ala Phe Ile Ser Tyr Ser
 100 105 110
 Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu Glu
 115 120 125
 Lys Glu Asp Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe Asp
 130 135 140
 Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys Ser
 145 150 155 160
 Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu Trp
 165 170 175
 Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu Asn
 180 185 190
 Ser Asp His Ile Ile Leu Ile Leu Leu Glu Pro Ile Pro Phe Tyr Cys
 195 200 205
 Ile Pro Thr Arg Tyr His Lys Leu Xaa Ala Leu Leu Glu Lys Lys Ala
 210 215 220
 Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Xaa Trp Ala
 225 230 235 240
 Asn Leu Arg Ala Ala Val Asn Val Asn Val Leu Ala Thr Arg Glu Met
 245 250 255
 Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly Ser
 260 265 270
 Thr Ile Xaa Leu Met Arg Thr Asp Cys Xaa
 275 280

<210> 33
 <211> 1173
 <212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised
Homo sapiens

<220>

<221> CDS

<222> (1)..(1008)

<220>

<221> misc feature

<222> (285)

<223> Xaa translation depends on genetic code

<400> 33
ctg cct gct ggc acc cgg ctc cgg agg ctg gat gtc agc tgc aac agc 48
Leu Pro Ala Gly Thr Arg Leu Arg Arg Leu Asp Val Ser Cys Asn Ser
1 5 10 15
atc agc ttc gtg gcc ccc ggc ttc ttt tcc aag gcc aag gag ctg cga 96
Ile Ser Phe Val Ala Pro Gly Phe Phe Ser Lys Ala Lys Glu Leu Arg
20 25 30
gag ctc aac ctt agc gcc aac gcc ctc aag aca gtg gac cac tcc tgg 144
Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys Thr Val Asp His Ser Trp
35 40 45
ttt ggg ccc ctg gcg agt gcc ctg caa ata cta gat gta agc gcc aac 192
Phe Gly Pro Leu Ala Ser Ala Leu Gln Ile Leu Asp Val Ser Ala Asn
50 55 60
cct ctg cac tgc gcc tgt ggg gcg gcc ttt atg gac ttc ctg ctg gag 240
Pro Leu His Cys Ala Cys Gly Ala Ala Phe Met Asp Phe Leu Leu Glu
65 70 75 80
gtg cag gct gcc gtg ccc ggt ctg ccc agc cgg gtg aag tgt ggc agt 288
Val Gln Ala Ala Val Pro Gly Leu Pro Ser Arg Val Lys Cys Gly Ser
85 90 95
ccg ggc cag ctc cag ggc ctc agc atc ttt gca cag gac ctg cgc ctc 336
Pro Gly Gln Leu Gln Gly Leu Ser Ile Phe Ala Gln Asp Leu Arg Leu
100 105 110
tgc ctg gat gag gcc ctc tcc tgg gac tgt ttc gcc ctc tcg ctg ctg 384
Cys Leu Asp Glu Ala Leu Ser Trp Asp Cys Phe Ala Leu Ser Leu Leu
115 120 125
gct gtg gct ctg ggc ctg ggt gtg ccc atg ctg cat cac ctc tgt ggc 432
Ala Val Ala Leu Gly Leu Gly Val Pro Met Leu His His Leu Cys Gly
130 135 140
tgg gac ctc tgg tac tgc ttc cac ctg tgc ctg gcc tgg ctt ccc tgg 480
Trp Asp Leu Trp Tyr Cys Phe His Leu Cys Leu Ala Trp Leu Pro Trp

145	150	155	160	
cgg ggg cgg caa agt ggg cga gat gag gat gcc ctg ccc tac gat gcc				528
Arg Gly Arg Gln Ser Gly Arg Asp Glu Asp Ala Leu Pro Tyr Asp Ala				
	165	170	175	
ttc gtg gtc ttc gac aaa acg cag agc gca gtg gca gac tgg gtg tac				576
Phe Val Val Phe Asp Lys Thr Gln Ser Ala Val Ala Asp Trp Val Tyr				
	180	185	190	
aac gag ctt cgg ggg cag ctg gag gag tgc cgt ggg cgc tgg gca ctc				624
Asn Glu Leu Arg Gly Gln Leu Glu Glu Cys Arg Gly Arg Trp Ala Leu				
	195	200	205	
cgc ctg tgc ctg gag gaa cgc gac tgg ctg cct ggc aaa acc ctc ttt				672
Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly Lys Thr Leu Phe				
	210	215	220	
gag aac ctg tgg gcc tcg gtc tat ggc agc cgc aag acg ctg ttt gtg				720
Glu Asn Leu Trp Ala Ser Val Tyr Gly Ser Arg Lys Thr Leu Phe Val				
	225	230	235	
ctg gcc cac acg gac cgg gtc agt ggt ctc ttg cgc gcc agc ttc ctg				768
Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu Arg Ala Ser Phe Leu				
	245	250	255	
ctg gcc cag cag cgc ctg ctg gag gac cgc aag gac gtc gtg gtg ctg				816
Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp Val Val Val Leu				
	260	265	270	
gtg atc ctg agc cct gac ggc cgc cgc tcc cgc tac gkg cgg ctg cgc				864
Val Ile Leu Ser Pro Asp Gly Arg Arg Ser Arg Tyr Xaa Arg Leu Arg				
	275	280	285	
cag cgc ctc tgc cgc cag agt gtc ctc ctc tgg ccc cac cag ccc agt				912
Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro His Gln Pro Ser				
	290	295	300	
ggt cag cgc agc ttc tgg gcc cag ctg ggc atg gcc ctg acc agg gac				960
Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly Met Ala Leu Thr Arg Asp				
	305	310	315	
aac cac cac ttc tat aac cgg aac ttc tgc cag gga ccc acg gcc gaa				1008
Asn His His Phe Tyr Asn Arg Asn Phe Cys Gln Gly Pro Thr Ala Glu				
	325	330	335	
tagccgtgag ccggaatcct gcacggtgcc acctccacac tcacctcacc tctgcctgcc				1068
tggtctgacc ctcccctgct cgcctccctc accccacacc tgacacagag caggcactca				1128
ataaatgcta ccgaaggcta aaaaaaaaaa aaaaaaaaaa aanna				1173

<210> 34
<211> 336
<212> PRT
<213> Unknown

<400> 34
Leu Pro Ala Gly Thr Arg Leu Arg Arg Leu Asp Val Ser Cys Asn Ser
1 5 10 15

Ile Ser Phe Val Ala Pro Gly Phe Phe Ser Lys Ala Lys Glu Leu Arg
20 25 30

Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys Thr Val Asp His Ser Trp
35 40 45

Phe Gly Pro Leu Ala Ser Ala Leu Gln Ile Leu Asp Val Ser Ala Asn
50 55 60

Pro Leu His Cys Ala Cys Gly Ala Ala Phe Met Asp Phe Leu Leu Glu
65 70 75 80

Val Gln Ala Ala Val Pro Gly Leu Pro Ser Arg Val Lys Cys Gly Ser
85 90 95

Pro Gly Gln Leu Gln Gly Leu Ser Ile Phe Ala Gln Asp Leu Arg Leu
100 105 110

Cys Leu Asp Glu Ala Leu Ser Trp Asp Cys Phe Ala Leu Ser Leu Leu
115 120 125

Ala Val Ala Leu Gly Leu Gly Val Pro Met Leu His His Leu Cys Gly
130 135 140

Trp Asp Leu Trp Tyr Cys Phe His Leu Cys Leu Ala Trp Leu Pro Trp
145 150 155 160

Arg Gly Arg Gln Ser Gly Arg Asp Glu Asp Ala Leu Pro Tyr Asp Ala
165 170 175

Phe Val Val Phe Asp Lys Thr Gln Ser Ala Val Ala Asp Trp Val Tyr
180 185 190

Asn Glu Leu Arg Gly Gln Leu Glu Glu Cys Arg Gly Arg Trp Ala Leu
195 200 205

Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly Lys Thr Leu Phe
210 215 220

Glu Asn Leu Trp Ala Ser Val Tyr Gly Ser Arg Lys Thr Leu Phe Val
225 230 235 240

Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu Arg Ala Ser Phe Leu
245 250 255

Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp Val Val Val Leu
 260 265 270
 Val Ile Leu Ser Pro Asp Gly Arg Arg Ser Arg Tyr Xaa Arg Leu Arg
 275 280 285
 Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro His Gln Pro Ser
 290 295 300
 Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly Met Ala Leu Thr Arg Asp
 305 310 315 320
 Asn His His Phe Tyr Asn Arg Asn Phe Cys Gln Gly Pro Thr Ala Glu
 325 330 335

<210> 35
 <211> 497
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:rodent; surmised
 Mus musculus

<400> 35
 tggccacac ggaccgcgtc agtggcctcc tgcgcaccag cttcctgctg gctcagcagc 60
 gcctgttgga agaccgcaag gacgtggtgg tggttggtgat cctgcgtccg gatgccccac 120
 cgtcccgcta tgtgcgactg cgccagcgtc tctgccgcca gagtgtgctc ttctggcccc 180
 agcgacccaa cgggcagggg ggcttctggg ccagctgag tacagccctg actagggaca 240
 accgccactt ctataaccag aacttctgcc ggggacctac agcagaatag ctgagagcaa 300
 cagctggaaa cagctgcatt ttcattgtctg gttcccgagt tgctctgcct gccttgctct 360
 gtcttactac accgctattt ggcaagtgcg caatatatgc taccaagcca ccaggccac 420
 ggagcaaagg ttggctgtaa agggtagttt tcttcccatg catctttcag gagagtgaag 480
 atagacacca aaccac 497

<210> 36
 <211> 3099
 <212> DNA
 <213> Unknown

<220>
 <223> Description of Unknown Organism:primate; surmised
 Homo sapiens

<220>
<221> CDS
<222> (1)..(3096)

<220>
<221> mat_peptide
<222> (52)..(3096)

<220>
<221> misc_feature
<222> (725)
<223> Xaa translation depends on genetic code

<400> 36
atg ctg acc tgc att ttc ctg cta ata tct ggt tcc tgt gag tta tgc 48
Met Leu Thr Cys Ile Phe Leu Leu Ile Ser Gly Ser Cys Glu Leu Cys
-15 -10 -5

gcc gaa gaa aat ttt tct aga agc tat cct tgt gat gag aaa aag caa 96
Ala Glu Glu Asn Phe Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln
-1 5 10 15

aat gac tca gtt att gca gag tgc agc aat cgt cga cta cag gaa gtt 144
Asn Asp Ser Val Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val
20 25 30

ccc caa acg gtg ggc aaa tat gtg aca gaa cta gac ctg tct gat aat 192
Pro Gln Thr Val Gly Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn
35 40 45

ttc atc aca cac ata acg aat gaa tca ttt caa ggg ctg caa aat ctc 240
Phe Ile Thr His Ile Thr Asn Glu Ser Phe Gln Gly Leu Gln Asn Leu
50 55 60

act aaa ata aat cta aac cac aac ccc aat gta cag cac cag aac gga 288
Thr Lys Ile Asn Leu Asn His Asn Pro Asn Val Gln His Gln Asn Gly
65 70 75

aat ccc ggt ata caa tca aat ggc ttg aat atc aca gac ggg gca ttc 336
Asn Pro Gly Ile Gln Ser Asn Gly Leu Asn Ile Thr Asp Gly Ala Phe
80 85 90 95

ctc aac cta aaa aac cta agg gag tta ctg ctt gaa gac aac cag tta 384
Leu Asn Leu Lys Asn Leu Arg Glu Leu Leu Leu Glu Asp Asn Gln Leu
100 105 110

ccc caa ata ccc tct ggt ttg cca gag tct ttg aca gaa ctt agt cta 432
Pro Gln Ile Pro Ser Gly Leu Pro Glu Ser Leu Thr Glu Leu Ser Leu
115 120 125

att caa aac aat ata tac aac ata act aaa gag ggc att tca aga ctt 480
Ile Gln Asn Asn Ile Tyr Asn Ile Thr Lys Glu Gly Ile Ser Arg Leu
130 135 140

ca aac ttg aaa aat ctc tat ttg gcc tgg aac tgc tat ttt aac aaa	528
le Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn Cys Tyr Phe Asn Lys	
145 150 155	
tt tgc gag aaa act aac ata gaa gat gga gta ttt gaa acg ctg aca	576
al Cys Glu Lys Thr Asn Ile Glu Asp Gly Val Phe Glu Thr Leu Thr	
60 165 170 175	
at ttg gag ttg cta tca cta tct ttc aat tct ctt tca cat gtg cca	624
sn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu Ser His Val Pro	
180 185 190	
ccc aaa ctg cca agc tcc cta cgc aaa ctt ttt ctg agc aac acc cag	672
pro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu Ser Asn Thr Gln	
195 200 205	
atc aaa tac att agt gaa gaa gat ttc aag gga ttg ata aat tta aca	720
ile Lys Tyr Ile Ser Glu Glu Asp Phe Lys Gly Leu Ile Asn Leu Thr	
210 215 220	
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Leu Leu Asp Leu Ser Gly Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe	
225 230 235	
cca tgc gtg cct tgt gat ggt ggt gct tca att aat ata gat cgt ttt	816
Pro Lys Val Pro Cys Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe	
240 245 250 255	
gct ttt caa aac ttg acc caa ctt cga tac cta aac ctc tct agc act	864
Ala Phe Gln Asn Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr	
260 265 270	
tcc ctc agg aag att aat gct gcc tgg ttt aaa aat atg cct cat ctg	912
Ser Leu Arg Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu	
275 280 285	
aag gtg ctg gat ctt gaa ttc aac tat tta gtg gga gaa ata gcc tct	960
Lys Val Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly Glu Ile Ala Ser	
290 295 300	
ggg gca ttt tta acg atg ctg ccc cgc tta gaa ata ctt gac ttg tct	1008
Gly Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser	
305 310 315	
ttt aac tat ata aag ggg agt tat cca cag cat att aat att tcc aga	1056
Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser Arg	
320 325 330 335	
aac ttc tct aaa ctt ttg tct cta cgg gca ttg cat tta aga ggt tat	1104
Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg Gly Tyr	
340 345 350	

g	ttc	cag	gaa	ctc	aga	gaa	gat	gat	ttc	cag	ccc	ctg	atg	cag	ctt	1152
al	Phe	Gln	Glu	Leu	Arg	Glu	Asp	Asp	Phe	Gln	Pro	Leu	Met	Gln	Leu	
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ca	aac	tta	tcg	act	atc	aac	ttg	ggt	att	aat	ttt	att	aag	caa	atc	1200
ro	Asn	Leu	Ser	Thr	Ile	Asn	Leu	Gly	Ile	Asn	Phe	Ile	Lys	Gln	Ile	
		370					375					380				
at	ttc	aaa	ctt	ttc	caa	aat	ttc	tcc	aat	ctg	gaa	att	att	tac	ttg	1248
sp	Phe	Lys	Leu	Phe	Gln	Asn	Phe	Ser	Asn	Leu	Glu	Ile	Ile	Tyr	Leu	
		385				390					395					
ca	gaa	aac	aga	ata	tca	ccg	ttg	gta	aaa	gat	acc	cgg	cag	agt	tat	1296
er	Glu	Asn	Arg	Ile	Ser	Pro	Leu	Val	Lys	Asp	Thr	Arg	Gln	Ser	Tyr	
00					405					410					415	
ca	aat	agt	tcc	tct	ttt	caa	cgt	cat	atc	cgg	aaa	cga	cgc	tca	aca	1344
ala	Asn	Ser	Ser	Ser	Phe	Gln	Arg	His	Ile	Arg	Lys	Arg	Arg	Ser	Thr	
			420					425						430		
gat	ttt	gag	ttt	gac	cca	cat	tcg	aac	ttt	tat	cat	ttc	acc	cgt	cct	1392
Asp	Phe	Glu	Phe	Asp	Pro	His	Ser	Asn	Phe	Tyr	His	Phe	Thr	Arg	Pro	
			435					440					445			
tta	ata	aag	cca	caa	tgt	gct	gct	tat	gga	aaa	gcc	tta	gat	tta	agc	1440
Leu	Ile	Lys	Pro	Gln	Cys	Ala	Ala	Tyr	Gly	Lys	Ala	Leu	Asp	Leu	Ser	
		450					455					460				
ctc	aac	agt	att	ttc	ttc	att	ggg	cca	aac	caa	ttt	gaa	aat	ctt	cct	1488
Leu	Asn	Ser	Ile	Phe	Phe	Ile	Gly	Pro	Asn	Gln	Phe	Glu	Asn	Leu	Pro	
		465				470					475					
gac	att	gcc	tgt	tta	aat	ctg	tct	gca	aat	agc	aat	gct	caa	gtg	tta	1536
Asp	Ile	Ala	Cys	Leu	Asn	Leu	Ser	Ala	Asn	Ser	Asn	Ala	Gln	Val	Leu	
480					485					490					495	
agt	gga	act	gaa	ttt	tca	gcc	att	cct	cat	gtc	aaa	tat	ttg	gat	ttg	1584
Ser	Gly	Thr	Glu	Phe	Ser	Ala	Ile	Pro	His	Val	Lys	Tyr	Leu	Asp	Leu	
			500						505					510		
aca	aac	aat	aga	cta	gac	ttt	gat	aat	gct	agt	gct	ctt	act	gaa	ttg	1632
Thr	Asn	Asn	Arg	Leu	Asp	Phe	Asp	Asn	Ala	Ser	Ala	Leu	Thr	Glu	Leu	
			515					520					525			
tcc	gac	ttg	gaa	gtt	cta	gat	ctc	agc	tat	aat	tca	cac	tat	ttc	aga	1680
Ser	Asp	Leu	Glu	Val	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	His	Tyr	Phe	Arg	
		530					535					540				
ata	gca	ggc	gta	aca	cat	cat	cta	gaa	ttt	att	caa	aat	ttc	aca	aat	1728
Ile	Ala	Gly	Val	Thr	His	His	Leu	Glu	Phe	Ile	Gln	Asn	Phe	Thr	Asn	
		545				550					555					
cta	aaa	gtt	tta	aac	ttg	agc	cac	aac	aac	att	tat	act	tta	aca	gat	1776
Leu	Lys	Val	Leu	Asn	Leu	Ser	His	Asn	Asn	Ile	Tyr	Thr	Leu	Thr	Asp	

560	565	570	575	
aag tat aac ctg gaa agc aag tcc ctg gta gaa tta gtt ttc agt ggc Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe Ser Gly 580 585 590				1824
aat cgc ctt gac att ttg tgg aat gat gat gac aac agg tat atc tcc Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg Tyr Ile Ser 595 600 605				1872
att ttc aaa ggt ctc aag aat ctg aca cgt ctg gat tta tcc ctt aat Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp Leu Ser Leu Asn 610 615 620				1920
agg ctc aag cac atc cca aat gaa gca ttc ctt aat ttg cca gcg agt Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu Asn Leu Pro Ala Ser 625 630 635				1968
ctc act gaa cta cat ata aat gat aat atg tta aag ttt ttt aac tgg Leu Thr Glu Leu His Ile Asn Asp Asn Met Leu Lys Phe Phe Asn Trp 640 645 650 655				2016
aca tta ctc cag cag ttt cct cgt ctc gag ttg ctt gac tta cgt gga Thr Leu Leu Gln Gln Phe Pro Arg Leu Glu Leu Leu Asp Leu Arg Gly 660 665 670				2064
aac aaa cta ctc ttt tta act gat agc cta tct gac ttt aca tct tcc Asn Lys Leu Leu Phe Leu Thr Asp Ser Leu Ser Asp Phe Thr Ser Ser 675 680 685				2112
ctt cgg aca ctg ctg ctg agt cat aac agg att tcc cac cta ccc tct Leu Arg Thr Leu Leu Leu Ser His Asn Arg Ile Ser His Leu Pro Ser 690 695 700				2160
ggc ttt ctt tct gaa gtc agt agt ctg aag cac ctc gat tta agt tcc Gly Phe Leu Ser Glu Val Ser Ser Leu Lys His Leu Asp Leu Ser Ser 705 710 715				2208
aat ctg cta aaa aca atm aac aaa tcc gca ctt gaa act aag acc acc Asn Leu Leu Lys Thr Xaa Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr 720 725 730 735				2256
acc aaa tta tct atg ttg gaa cta cac gga aac ccc ttt gaa tgc acc Thr Lys Leu Ser Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr 740 745 750				2304
tgt gac att gga gat ttc cga aga tgg atg gat gaa cat ctg aat gtc Cys Asp Ile Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val 755 760 765				2352
aaa att ccc aga ctg gta gat gtc att tgt gcc agt cct ggg gat caa Lys Ile Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln 770 775 780				2400

aga ggg aag agt att gtg agt ctg gag cta aca act tgt gtt tca gat	2448
Arg Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp	
785 790 795	
gtc act gca gtg ata tta ttt ttc ttc acg ttc ttt atc acc acc atg	2496
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr Met	
800 805 810 815	
gtt atg ttg gct gcc ctg gct cac cat ttg ttt tac tgg gat gtt tgg	2544
Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp Val Trp	
820 825 830	
ttt ata tat aat gtg tgt tta gct aag tta aaa ggc tac agg tct ctt	2592
Phe Ile Tyr Asn Val Cys Leu Ala Lys Leu Lys Gly Tyr Arg Ser Leu	
835 840 845	
tcc aca tcc caa act ttc tat gat gct tac att tct tat gac acc aaa	2640
Ser Thr Ser Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr Asp Thr Lys	
850 855 860	
gat gcc tct gtt act gac tgg gtg ata aat gag ctg cgc tac cac ctt	2688
Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg Tyr His Leu	
865 870 875	
gaa gag agc cga gac aaa aac gtt ctc ctt tgt cta gag gag agg gat	2736
Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu Glu Arg Asp	
880 885 890 895	
tgg gac ccg gga ttg gcc atc atc gac aac ctc atg cag agc atc aac	2784
Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln Ser Ile Asn	
900 905 910	
caa agc aag aaa aca gta ttt gtt tta acc aaa aaa tat gca aaa agc	2832
Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr Ala Lys Ser	
915 920 925	
tgg aac ttt aaa aca gct ttt tac ttg gcc ttg cag agg cta atg ggt	2880
Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu Gln Arg Leu Met Gly	
930 935 940	
gag aac atg gat gtg att ata ttt atc ctg ctg gag cca gtg tta cag	2928
Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro Val Leu Gln	
945 950 955	
cat tct ccg tat ttg agg cta cgg cag cgg atc tgt aag agc tcc atc	2976
His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile	
960 965 970 975	
ctc cag tgg cct gac aac ccg aag gca gaa ggc ttg ttt tgg caa act	3024
Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr	
980 985 990	
ctg aga aat gtg gtc ttg act gaa aat gat tca cgg tat aac aat atg	3072

eu Arg Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met
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3099

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yr Val Asp Ser Ile Lys Gln Tyr
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211> 1032
212> PRT
213> Unknown

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Asn Asp Ser Val Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val
20 25 30

Pro Gln Thr Val Gly Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn
35 40 45

Phe Ile Thr His Ile Thr Asn Glu Ser Phe Gln Gly Leu Gln Asn Leu
50 55 60

Thr Lys Ile Asn Leu Asn His Asn Pro Asn Val Gln His Gln Asn Gly
65 70 75

Asn Pro Gly Ile Gln Ser Asn Gly Leu Asn Ile Thr Asp Gly Ala Phe
80 85 90 95

Leu Asn Leu Lys Asn Leu Arg Glu Leu Leu Leu Glu Asp Asn Gln Leu
100 105 110

Pro Gln Ile Pro Ser Gly Leu Pro Glu Ser Leu Thr Glu Leu Ser Leu
115 120 125

Ile Gln Asn Asn Ile Tyr Asn Ile Thr Lys Glu Gly Ile Ser Arg Leu
130 135 140

Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn Cys Tyr Phe Asn Lys
145 150 155

Val Cys Glu Lys Thr Asn Ile Glu Asp Gly Val Phe Glu Thr Leu Thr
160 165 170 175

Asn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu Ser His Val Pro
180 185 190

ro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu Ser Asn Thr Gln
 195 200 205
 le Lys Tyr Ile Ser Glu Glu Asp Phe Lys Gly Leu Ile Asn Leu Thr
 210 215 220
 leu Leu Asp Leu Ser Gly Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe
 225 230 235
 pro Cys Val Pro Cys Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe
 240 245 250 255
 ala Phe Gln Asn Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr
 260 265 270
 Ser Leu Arg Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu
 275 280 285
 Lys Val Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly Glu Ile Ala Ser
 290 295 300
 Gly Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser
 305 310 315
 Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser Arg
 320 325 330 335
 Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg Gly Tyr
 340 345 350
 Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro Leu Met Gln Leu
 355 360 365
 Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe Ile Lys Gln Ile
 370 375 380
 Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu Glu Ile Ile Tyr Leu
 385 390 395
 Ser Glu Asn Arg Ile Ser Pro Leu Val Lys Asp Thr Arg Gln Ser Tyr
 400 405 410 415
 Ala Asn Ser Ser Ser Phe Gln Arg His Ile Arg Lys Arg Arg Ser Thr
 420 425 430
 Asp Phe Glu Phe Asp Pro His Ser Asn Phe Tyr His Phe Thr Arg Pro
 435 440 445
 Leu Ile Lys Pro Gln Cys Ala Ala Tyr Gly Lys Ala Leu Asp Leu Ser
 450 455 460
 Leu Asn Ser Ile Phe Phe Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro
 465 470 475

Asp Ile Ala Cys Leu Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu 480 485 490 495
 Ser Gly Thr Glu Phe Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu 500 505 510
 Thr Asn Asn Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu 515 520 525
 Ser Asp Leu Glu Val Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg 530 535 540
 Ile Ala Gly Val Thr His His Leu Glu Phe Ile Gln Asn Phe Thr Asn 545 550 555
 Leu Lys Val Leu Asn Leu Ser His Asn Asn Ile Tyr Thr Leu Thr Asp 560 565 570 575
 Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe Ser Gly 580 585 590
 Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg Tyr Ile Ser 595 600 605
 Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp Leu Ser Leu Asn 610 615 620
 Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu Asn Leu Pro Ala Ser 625 630 635
 Leu Thr Glu Leu His Ile Asn Asp Asn Met Leu Lys Phe Phe Asn Trp 640 645 650 655
 Thr Leu Leu Gln Gln Phe Pro Arg Leu Glu Leu Leu Asp Leu Arg Gly 660 665 670
 Asn Lys Leu Leu Phe Leu Thr Asp Ser Leu Ser Asp Phe Thr Ser Ser 675 680 685
 Leu Arg Thr Leu Leu Leu Ser His Asn Arg Ile Ser His Leu Pro Ser 690 695 700
 Gly Phe Leu Ser Glu Val Ser Ser Leu Lys His Leu Asp Leu Ser Ser 705 710 715
 Asn Leu Leu Lys Thr Xaa Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr 720 725 730 735
 Thr Lys Leu Ser Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr 740 745 750
 Cys Asp Ile Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val 755 760 765

Lys Ile Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln
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 Arg Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp
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 800 805 810 815
 Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp Val Trp
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 Phe Ile Tyr Asn Val Cys Leu Ala Lys Leu Lys Gly Tyr Arg Ser Leu
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 Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr Asp Thr Lys
 850 855 860
 Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg Tyr His Leu
 865 870 875
 Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu Glu Arg Asp
 880 885 890 895
 Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln Ser Ile Asn
 900 905 910
 Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr Ala Lys Ser
 915 920 925
 Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu Gln Arg Leu Met Gly
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 Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro Val Leu Gln
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 1010 1015

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 <213> Unknown

220>
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Homo sapiens

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221> CDS
222> (111)..(2543)

220>
221> mat_peptide
222> (168)..(2543)

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ttcttcatca ttcatatgag gaaataagtg gtaaaatcct tggaaataca atg aga 116
Met Arg
ctc atc aga aac att tac ata ttt tgt agt att gtt atg aca gca gag 164
Leu Ile Arg Asn Ile Tyr Ile Phe Cys Ser Ile Val Met Thr Ala Glu
-15 -10 -5
ggg gat gct cca gag ctg cca gaa gaa agg gaa ctg atg acc aac tgc 212
Gly Asp Ala Pro Glu Leu Pro Glu Glu Arg Glu Leu Met Thr Asn Cys
-1 1 5 10 15
tcc aac atg tct cta aga aag gtt ccc gca gac ttg acc cca gcc aca 260
Ser Asn Met Ser Leu Arg Lys Val Pro Ala Asp Leu Thr Pro Ala Thr
20 25 30
acg aca ctg gat tta tcc tat aac ctc ctt ttt caa ctc cag agt tca 308
Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu Phe Gln Leu Gln Ser Ser
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gat ttt cat tct gtc tcc aaa ctg aga gtt ttg att cta tgc cat aac 356
Asp Phe His Ser Val Ser Lys Leu Arg Val Leu Ile Leu Cys His Asn
50 55 60
aga att caa cag ctg gat ctc aaa acc ttt gaa ttc aac aag gag tta 404
Arg Ile Gln Gln Leu Asp Leu Lys Thr Phe Glu Phe Asn Lys Glu Leu
65 70 75
aga tat tta gat ttg tct aat aac aga ctg aag agt gta act tgg tat 452
Arg Tyr Leu Asp Leu Ser Asn Asn Arg Leu Lys Ser Val Thr Trp Tyr
80 85 90 95
tta ctg gca ggt ctc agg tat tta gat ctt tct ttt aat gac ttt gac 500
Leu Leu Ala Gly Leu Arg Tyr Leu Asp Leu Ser Phe Asn Asp Phe Asp
100 105 110
acc atg cct atc tgt gag gaa gct ggc aac atg tca cac ctg gaa atc 548
Thr Met Pro Ile Cys Glu Glu Ala Gly Asn Met Ser His Leu Glu Ile

115

120

125

cta ggt ttg agt ggg gca aaa ata caa aaa tca gat ttc cag aaa att 596
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 130 135 140

gct cat ctg cat cta aat act gtc ttc tta gga ttc aga act ctt cct 644
 Ala His Leu His Leu Asn Thr Val Phe Leu Gly Phe Arg Thr Leu Pro
 145 150 155

cat tat gaa gaa ggt agc ctg ccc atc tta aac aca aca aaa ctg cac 692
 His Tyr Glu Glu Gly Ser Leu Pro Ile Leu Asn Thr Thr Lys Leu His
 160 165 170 175

att gtt tta cca atg gac aca aat ttc tgg gtt ctt ttg cgt gat gga 740
 Ile Val Leu Pro Met Asp Thr Asn Phe Trp Val Leu Leu Arg Asp Gly
 180 185 190

atc aag act tca aaa ata tta gaa atg aca aat ata gat ggc aaa agc 788
 Ile Lys Thr Ser Lys Ile Leu Glu Met Thr Asn Ile Asp Gly Lys Ser
 195 200 205

caa ttt gta agt tat gaa atg caa cga aat ctt agt tta gaa aat gct 836
 Gln Phe Val Ser Tyr Glu Met Gln Arg Asn Leu Ser Leu Glu Asn Ala
 210 215 220

aag aca tcg gtt cta ttg ctt aat aaa gtt gat tta ctc tgg gac gac 884
 Lys Thr Ser Val Leu Leu Leu Asn Lys Val Asp Leu Leu Trp Asp Asp
 225 230 235

ctc ttc ctt atc tta caa ttt gtt tgg cat aca tca gtg gaa cac ttt 932
 Leu Phe Leu Ile Leu Gln Phe Val Trp His Thr Ser Val Glu His Phe
 240 245 250 255

cag atc cga aat gtg act ttt ggt ggt aag gct tat ctt gac cac aat 980
 Gln Ile Arg Asn Val Thr Phe Gly Gly Lys Ala Tyr Leu Asp His Asn
 260 265 270

tca ttt gac tac tca aat act gta atg aga act ata aaa ttg gag cat 1028
 Ser Phe Asp Tyr Ser Asn Thr Val Met Arg Thr Ile Lys Leu Glu His
 275 280 285

gta cat ttc aga gtg ttt tac att caa cag gat aaa atc tat ttg ctt 1076
 Val His Phe Arg Val Phe Tyr Ile Gln Gln Asp Lys Ile Tyr Leu Leu
 290 295 300

ttg acc aaa atg gac ata gaa aac ctg aca ata tca aat gca caa atg 1124
 Leu Thr Lys Met Asp Ile Glu Asn Leu Thr Ile Ser Asn Ala Gln Met
 305 310 315

cca cac atg ctt ttc ccg aat tat cct acg aaa ttc caa tat tta aat 1172
 Pro His Met Leu Phe Pro Asn Tyr Pro Thr Lys Phe Gln Tyr Leu Asn
 320 325 330 335

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Phe Ala Asn Asn Ile Leu Thr Asp Glu Leu Phe Lys Arg Thr Ile Gln	
340 345 350	
ctg cct cac ttg aaa act ctc att ttg aat ggc aat aaa ctg gag aca	1268
Leu Pro His Leu Lys Thr Leu Ile Leu Asn Gly Asn Lys Leu Glu Thr	
355 360 365	
ctt tct tta gta agt tgc ttt gct aac aac aca ccc ttg gaa cac ttg	1316
Leu Ser Leu Val Ser Cys Phe Ala Asn Asn Thr Pro Leu Glu His Leu	
370 375 380	
gat ctg agt caa aat cta tta caa cat aaa aat gat gaa aat tgc tca	1364
Asp Leu Ser Gln Asn Leu Leu Gln His Lys Asn Asp Glu Asn Cys Ser	
385 390 395	
tgg cca gaa act gtg gtc aat atg aat ctg tca tac aat aaa ttg tct	1412
Trp Pro Glu Thr Val Val Asn Met Asn Leu Ser Tyr Asn Lys Leu Ser	
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gat tct gtc ttc agg tgc ttg ccc aaa agt att caa ata ctt gac cta	1460
Asp Ser Val Phe Arg Cys Leu Pro Lys Ser Ile Gln Ile Leu Asp Leu	
420 425 430	
aat aat aac caa atc caa act gta cct aaa gag act att cat ctg atg	1508
Asn Asn Asn Gln Ile Gln Thr Val Pro Lys Glu Thr Ile His Leu Met	
435 440 445	
gca tta cga gaa cta aat att gca ttt aat ttt cta act gat ctc cct	1556
Ala Leu Arg Glu Leu Asn Ile Ala Phe Asn Phe Leu Thr Asp Leu Pro	
450 455 460	
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Gly Cys Ser His Phe Ser Arg Leu Ser Val Leu Asn Ile Glu Met Asn	
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Phe Ile Leu Ser Pro Ser Leu Asp Phe Val Gln Ser Cys Gln Glu Val	
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Lys Thr Leu Asn Ala Gly Arg Asn Pro Phe Arg Cys Thr Cys Glu Leu	
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Lys Asn Phe Ile Gln Leu Glu Thr Tyr Ser Glu Val Met Met Val Gly	
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Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly Thr	
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ctt	cga	gct	gct	att	aat	ggt	aat	gta	tta	gcc	acc	aga	gaa	atg	tat	2468	
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 Ile Ser Leu Met Arg Thr Asp Cys Leu
 785 790

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Ser Ser Asp Phe His Ser Val Ser Lys Leu Arg Val Leu Ile Leu Cys
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His Asn Arg Ile Gln Gln Leu Asp Leu Lys Thr Phe Glu Phe Asn Lys
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Glu Leu Arg Tyr Leu Asp Leu Ser Asn Asn Arg Leu Lys Ser Val Thr

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85

90

Trp Tyr Leu Leu Ala Gly Leu Arg Tyr Leu Asp Leu Ser Phe Asn Asp
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Phe Asp Thr Met Pro Ile Cys Glu Glu Ala Gly Asn Met Ser His Leu
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Lys Ile Ala His Leu His Leu Asn Thr Val Phe Leu Gly Phe Arg Thr
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Leu Pro His Tyr Glu Glu Gly Ser Leu Pro Ile Leu Asn Thr Thr Lys
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Leu His Ile Val Leu Pro Met Asp Thr Asn Phe Trp Val Leu Leu Arg
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Asp Gly Ile Lys Thr Ser Lys Ile Leu Glu Met Thr Asn Ile Asp Gly
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Lys Ser Gln Phe Val Ser Tyr Glu Met Gln Arg Asn Leu Ser Leu Glu
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Asp Asp Leu Phe Leu Ile Leu Gln Phe Val Trp His Thr Ser Val Glu
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Gln Met Pro His Met Leu Phe Pro Asn Tyr Pro Thr Lys Phe Gln Tyr
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Ile Gln Leu Pro His Leu Lys Thr Leu Ile Leu Asn Gly Asn Lys Leu
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Glu Thr Leu Ser Leu Val Ser Cys Phe Ala Asn Asn Thr Pro Leu Glu

370

375

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 Gln Glu Gln Leu Lys Arg Asn Val Arg Phe His Ala Phe Ile Ser Tyr
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 Ser Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu
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 Glu Lys Glu Asp Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe
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Asp Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys
655 660 665

Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu
670 675 680 685

Trp Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu
690 695 700

Asn Ser Asp His Ile Ile Leu Ile Leu Glu Pro Ile Pro Phe Tyr
705 710 715

Cys Ile Pro Thr Arg Tyr His Lys Leu Lys Ala Leu Leu Glu Lys Lys
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735 740 745

Ala Asn Leu Arg Ala Ala Ile Asn Val Asn Val Leu Ala Thr Arg Glu
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Tyr Ile Ala Glu Leu Gln Val Ser Asp Met Ser Phe Leu Ser Glu Leu	
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Thr Val Leu Arg Leu Ser His Asn Arg Ile Gln Leu Leu Asp Leu Ser	
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Val Phe Lys Phe Asn Gln Asp Leu Glu Tyr Leu Asp Leu Ser His Asn	
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Gln Leu Gln Lys Ile Ser Cys His Pro Ile Val Ser Phe Arg His Leu	
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Asp Leu Ser Phe Asn Asp Phe Lys Ala Leu Pro Ile Cys Lys Glu Phe	
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Gln Lys Leu Asp Leu Leu Pro Ile Ala His Leu His Leu Ser Tyr Ile	
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ctt ctg gat tta aga aat tat tat ata aaa gaa aat gag aca gaa agt	637
Leu Leu Asp Leu Arg Asn Tyr Tyr Ile Lys Glu Asn Glu Thr Glu Ser	
145 150 155	
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Leu Gln Ile Leu Asn Ala Lys Thr Leu His Leu Val Phe His Pro Thr	
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Ser Leu Phe Ala Ile Gln Val Asn Ile Ser Val Asn Thr Leu Gly Cys	

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Ala	His	His	Asn	Leu	Phe	His	Glu	Gly	Ser	Asn	Asn	Leu	Ile	Leu	Ile		
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Leu	Leu	Glu	Pro	Ile	Pro	Gln	Asn	Ser	Ile	Pro	Asn	Lys	Tyr	His	Lys		
	705					710					715						
ctg	taag	gct	ctc	atg	acg	cag	cgg	act	tat	ttg	cag	tgg	ccc	aag	gag	2365	
Leu	Lys	Ala	Leu	Met	Thr	Gln	Arg	Thr	Tyr	Leu	Gln	Trp	Pro	Lys	Glu		
720					725					730					735		
aaa	agc	aaa	cgt	ggg	ctc	ttt	tgg	gct	aac	att	aga	gcc	gct	ttt	aat	2413	
Lys	Ser	Lys	Arg	Gly	Leu	Phe	Trp	Ala	Asn	Ile	Arg	Ala	Ala	Phe	Asn		
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atg	aaa	tta	aca	cta	gtc	act	gaa	aac	aat	gat	gtg	aaa	tct			2455	
Met	Lys	Leu	Thr	Leu	Val	Thr	Glu	Asn	Asn	Asp	Val	Lys	Ser				
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Glu	Phe	Ala	Val	Asp	Lys	Ser	Lys	Arg	Gly	Leu	Ile	His	Val	Pro	Lys	
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Asp	Leu	Pro	Leu	Lys	Thr	Lys	Val	Leu	Asp	Met	Ser	Gln	Asn	Tyr	Ile	
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Ala	Glu	Leu	Gln	Val	Ser	Asp	Met	Ser	Phe	Leu	Ser	Glu	Leu	Thr	Val	
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Lys	Phe	Asn	Gln	Asp	Leu	Glu	Tyr	Leu	Asp	Leu	Ser	His	Asn	Gln	Leu	
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Gln	Lys	Ile	Ser	Cys	His	Pro	Ile	Val	Ser	Phe	Arg	His	Leu	Asp	Leu	
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Ser	Phe	Asn	Asp	Phe	Lys	Ala	Leu	Pro	Ile	Cys	Lys	Glu	Phe	Gly	Asn	
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Leu	Ser	Gln	Leu	Asn	Phe	Leu	Gly	Leu	Ser	Ala	Met	Lys	Leu	Gln	Lys	
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Leu	Asp	Leu	Leu	Pro	Ile	Ala	His	Leu	His	Leu	Ser	Tyr	Ile	Leu	Leu	
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Asp	Leu	Arg	Asn	Tyr	Tyr	Ile	Lys	Glu	Asn	Glu	Thr	Glu	Ser	Leu	Gln	
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Ile	Leu	Asn	Ala	Lys	Thr	Leu	His	Leu	Val	Phe	His	Pro	Thr	Ser	Leu	
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Phe	Ala	Ile	Gln	Val	Asn	Ile	Ser	Val	Asn	Thr	Leu	Gly	Cys	Leu	Gln	
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Leu	Thr	Asn	Ile	Lys	Leu	Asn	Asp	Asp	Asn	Cys	Gln	Val	Phe	Ile	Lys	
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Phe	Leu	Ser	Glu	Leu	Thr	Arg	Gly	Pro	Thr	Leu	Leu	Asn	Phe	Thr	Leu	
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Leu	Trp	Pro	Lys	Pro	Val	Glu	Tyr	Leu	Asn	Ile	Tyr	Asn	Leu	Thr	Ile				
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Ile	Glu	Ser	Ile	Arg	Glu	Glu	Asp	Phe	Thr	Tyr	Ser	Lys	Thr	Thr	Leu				
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Lys	Ala	Leu	Thr	Ile	Glu	His	Ile	Thr	Asn	Gln	Val	Phe	Leu	Phe	Ser				
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Ser	Thr	Phe	Lys	Phe	Leu	Asn	Phe	Thr	Gln	Asn	Val	Phe	Thr	Asp	Ser				
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Leu	Asn	Leu	Ser	Ser	Asn	Met	Leu	Thr	Asp	Ser	Val	Phe	Arg	Cys	Leu				
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Pro	Pro	Arg	Ile	Lys	Val	Leu	Asp	Leu	His	Ser	Asn	Lys	Ile	Lys	Ser				
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Val	Pro	Lys	Gln	Val	Val	Lys	Leu	Glu	Ala	Leu	Gln	Glu	Leu	Asn	Val				
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Ala	Phe	Asn	Ser	Leu	Thr	Asp	Leu	Pro	Gly	Cys	Gly	Ser	Phe	Ser	Ser				
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Asp	Phe	Phe	Gln	Ser	Cys	Gln	Lys	Met	Arg	Ser	Ile	Lys	Ala	Gly	Asp				
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Asn	Pro	Phe	Gln	Cys	Thr	Cys	Glu	Leu	Arg	Glu	Phe	Val	Lys	Asn	Ile				
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Asp	Gln	Val	Ser	Ser	Glu	Val	Leu	Glu	Gly	Trp	Pro	Asp	Ser	Tyr	Lys				

515	520	525
Cys Asp Tyr Pro Glu Ser Tyr Arg Gly Ser Pro Leu Lys Asp Phe His 530 535 540 545		
Met Ser Glu Leu Ser Cys Asn Ile Thr Leu Leu Ile Val Thr Ile Gly 550 555 560		
Ala Thr Met Leu Val Leu Ala Val Thr Val Thr Ser Leu Cys Ile Tyr 565 570 575		
Leu Asp Leu Pro Trp Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr 580 585 590		
Arg Arg Arg Ala Arg Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu 595 600 605		
Gln Phe His Ala Phe Ile Ser Tyr Ser Glu His Asp Ser Ala Trp Val 610 615 620 625		
Lys Ser Glu Leu Val Pro Tyr Leu Glu Lys Glu Asp Ile Gln Ile Cys 630 635 640		
Leu His Glu Arg Asn Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile 645 650 655		
Ile Asn Cys Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro 660 665 670		
Asn Phe Val Gln Ser Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His 675 680 685		
His Asn Leu Phe His Glu Gly Ser Asn Asn Leu Ile Leu Ile Leu Leu 690 695 700 705		
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Ala Leu Met Thr Gln Arg Thr Tyr Leu Gln Trp Pro Lys Glu Lys Ser 725 730 735		
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Homo sapiens

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His Thr Ala Leu Pro Pro Pro Gln Gly Phe Cys Arg Ser Ala Leu His
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Pro Leu Ser Leu Leu Val Gln Ala Ile Met Leu Ala Met Thr Leu Ala
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1 5 10 15

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Leu Val Asn Cys Asn Trp Leu Phe Leu Lys Ser Val Pro His Phe Ser
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Met Ala Ala Pro Arg Gly Asn Val Thr Ser Leu Ser Leu Ser Ser Asn
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cgc atc cac cac ctc cat gat tct gac ttt gcc cac ctg ccc agc ctg 336
Arg Ile His His Leu His Asp Ser Asp Phe Ala His Leu Pro Ser Leu
50 55 60

cgg cat ctc aac ctc aag tgg aac tgc ccg ccg gtt ggc ctc agc ccc 384
Arg His Leu Asn Leu Lys Trp Asn Cys Pro Pro Val Gly Leu Ser Pro
65 70 75 80

atg cac ttc ccc tgc cac atg acc atc gag ccc agc acc ttc ttg gct 432
Met His Phe Pro Cys His Met Thr Ile Glu Pro Ser Thr Phe Leu Ala
85 90 95

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Val Pro Thr Leu Glu Glu Leu Asn Leu Ser Tyr Asn Asn Ile Met Thr
100 105 110

gtg cct gcg ctg ccc aaa tcc ctc ata tcc ctg tcc ctc agc cat acc 528

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Asn	Ile	Leu	Met	Leu	Asp	Ser	Ala	Ser	Leu	Ala	Gly	Leu	His	Ala	Leu		
	130					135					140						
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Arg	Phe	Leu	Phe	Met	Asp	Gly	Asn	Cys	Tyr	Tyr	Lys	Asn	Pro	Cys	Arg		
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Gln	Ala	Leu	Glu	Val	Ala	Pro	Gly	Ala	Leu	Leu	Gly	Leu	Gly	Asn	Leu		
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acc	cac	ctg	tca	ctc	aag	tac	aac	aac	ctc	act	gtg	gtg	ccc	cgc	aac	720	
Thr	His	Leu	Ser	Leu	Lys	Tyr	Asn	Asn	Leu	Thr	Val	Val	Pro	Arg	Asn		
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Leu	Pro	Ser	Ser	Leu	Glu	Tyr	Leu	Leu	Leu	Ser	Tyr	Asn	Arg	Ile	Val		
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Met	Glu	Cys	Pro	Arg	His	Phe	Pro	Gln	Leu	His	Pro	Asp	Thr	Phe	Ser		
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335

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Gln	Thr	Leu	Arg	Leu	Gln	Met	Asn	Phe	Ile	Asn	Gln	Ala	Gln	Leu	Gly	
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Ile	Phe	Arg	Ala	Phe	Pro	Gly	Leu	Arg	Tyr	Val	Asp	Leu	Ser	Asp	Asn	
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Arg	Ile	Ser	Gly	Ala	Ser	Glu	Leu	Thr	Ala	Thr	Met	Gly	Glu	Ala	Asp	
				405					410					415		
gga	ggg	gag	aag	gtc	tgg	ctg	cag	cct	ggg	gac	ctt	gct	ccg	gcc	cca	1440
Gly	Gly	Glu	Lys	Val	Trp	Leu	Gln	Pro	Gly	Asp	Leu	Ala	Pro	Ala	Pro	
			420					425				430				
gtg	gac	act	ccc	agc	tct	gaa	gac	ttc	agg	ccc	aac	tgc	agc	acc	ctc	1488
Val	Asp	Thr	Pro	Ser	Ser	Glu	Asp	Phe	Arg	Pro	Asn	Cys	Ser	Thr	Leu	
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Asn	Phe	Thr	Leu	Asp	Leu	Ser	Arg	Asn	Asn	Leu	Val	Thr	Val	Gln	Pro	
						455					460					
gag	atg	ttt	gcc	cag	ctc	tcg	cac	ctg	cag	tgc	ctg	cgc	ctg	agc	cac	1584
Glu	Met	Phe	Ala	Gln	Leu	Ser	His	Leu	Gln	Cys	Leu	Arg	Leu	Ser	His	
					470					475					480	
aac	tgc	atc	tcg	cag	gca	gtc	aat	ggc	tcc	cag	ttc	ctg	ccg	ctg	acc	1632
Asn	Cys	Ile	Ser	Gln	Ala	Val	Asn	Gly	Ser	Gln	Phe	Leu	Pro	Leu	Thr	
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ggg	ctg	cag	gtg	cta	gac	ctg	tcc	cac	aat	aag	ctg	gac	ctc	tac	cac	1680
Gly	Leu	Gln	Val	Leu	Asp	Leu	Ser	His	Asn	Lys	Leu	Asp	Leu	Tyr	His	
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gag	cac	tca	ttc	acg	gag	cta	cca	cga	ctg	gag	gcc	ctg	gac	ctc	agc	1728
Glu	His	Ser	Phe	Thr	Glu	Leu	Pro	Arg	Leu	Glu	Ala	Leu	Asp	Leu	Ser	
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Ala	Leu	Asp	Phe	Ser	Gly	Asn	Ala	Leu	Gly	His	Met	Trp	Ala	Glu	Gly	
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Asp	Leu	Tyr	Leu	His	Phe	Phe	Gln	Gly	Leu	Ser	Gly	Leu	Ile	Trp	Leu	
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625					630				635						640	
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Ala	Phe	Phe	Lys	Trp	Trp	Ser	Leu	His	Phe	Leu	Pro	Lys	Leu	Glu	Val	
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Leu	Asp	Leu	Ala	Gly	Asn	Gln	Leu	Lys	Ala	Leu	Thr	Asn	Gly	Ser	Leu	
			660					665					670			
cct	gct	ggc	acc	cgg	ctc	cgg	agg	ctg	gat	gtc	agc	tgc	aac	agc	atc	2208
Pro	Ala	Gly	Thr	Arg	Leu	Arg	Arg	Leu	Asp	Val	Ser	Cys	Asn	Ser	Ile	
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Ser	Phe	Val	Ala	Pro	Gly	Phe	Phe	Ser	Lys	Ala	Lys	Glu	Leu	Arg	Glu	
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Gly	Pro	Leu	Ala	Ser	Ala	Leu	Gln	Ile	Leu	Asp	Val	Ser	Ala	Asn	Pro	
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Leu	His	Cys	Ala	Cys	Gly	Ala	Ala	Phe	Met	Asp	Phe	Leu	Leu	Glu	Val	
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Gln	Ala	Ala	Val	Pro	Gly	Leu	Pro	Ser	Arg	Val	Lys	Cys	Gly	Ser	Pro		
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	770					775					780						
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Leu	Asp	Glu	Ala	Leu	Ser	Trp	Asp	Cys	Phe	Ala	Leu	Ser	Leu	Leu	Ala		
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gtg	gct	ctg	ggc	ctg	ggg	gtg	ccc	atg	ctg	cat	cac	ctc	tgt	ggc	tgg	2592	
Val	Ala	Leu	Gly	Leu	Gly	Val	Pro	Met	Leu	His	His	Leu	Cys	Gly	Trp		
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gac	ctc	tgg	tac	tgc	ttc	cac	ctg	tgc	ctg	gcc	tgg	ctt	ccc	tgg	cgg	2640	
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Gly	Arg	Gln	Ser	Gly	Arg	Asp	Glu	Asp	Ala	Leu	Pro	Tyr	Asp	Ala	Phe		
	835						840					845					
gtg	gtc	ttc	gac	aaa	acg	cag	agc	gca	gtg	gca	gac	tgg	gtg	tac	aac	2736	
Val	Val	Phe	Asp	Lys	Thr	Gln	Ser	Ala	Val	Ala	Asp	Trp	Val	Tyr	Asn		
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gag	ttt	cgg	ggg	cag	ctg	gag	gag	tgc	cgt	ggg	cgc	tgg	gca	ctc	cgc	2784	
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				885					890					895			
aac	ctg	tgg	gcc	tgc	gtc	tat	ggc	agc	cgc	aag	acg	ctg	ttt	gtg	ctg	2880	
Asn	Leu	Trp	Ala	Ser	Val	Tyr	Gly	Ser	Arg	Lys	Thr	Leu	Phe	Val	Leu		
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gcc	cac	acg	gac	cgg	gtc	agt	ggg	ctc	ttg	cgc	gcc	agc	ttc	ctg	ctg	2928	
Ala	His	Thr	Asp	Arg	Val	Ser	Gly	Leu	Leu	Arg	Ala	Ser	Phe	Leu	Leu		
			915				920					925					
gcc	cag	cag	cgc	ctg	ctg	gag	gac	cgc	aag	gac	gtc	gtg	gtg	ctg	gtg	2976	
Ala	Gln	Gln	Arg	Leu	Leu	Glu	Asp	Arg	Lys	Asp	Val	Val	Val	Leu	Val		
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Ile	Leu	Ser	Pro	Asp	Gly	Arg	Arg	Ser	Arg	Tyr	Val	Arg	Leu	Arg	Gln		
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cgc	ctc	tgc	cgc	cag	agt	gtc	ctc	ctc	tgg	ccc	cac	cag	ccc	agt	ggg	3072	
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 980 985 990

cac cac ttc tat aac cgg aac ttc tgc cag gga ccc acg gcc gaa tag 3168
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Leu Gly Thr Leu Pro Ala Phe Leu Pro Cys Glu Leu Gln Pro His Gly
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Leu Val Asn Cys Asn Trp Leu Phe Leu Lys Ser Val Pro His Phe Ser
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Met Ala Ala Pro Arg Gly Asn Val Thr Ser Leu Ser Leu Ser Ser Asn
 35 40 45

Arg Ile His His Leu His Asp Ser Asp Phe Ala His Leu Pro Ser Leu
 50 55 60

Arg His Leu Asn Leu Lys Trp Asn Cys Pro Pro Val Gly Leu Ser Pro
 65 70 75 80

Met His Phe Pro Cys His Met Thr Ile Glu Pro Ser Thr Phe Leu Ala
 85 90 95

Val Pro Thr Leu Glu Glu Leu Asn Leu Ser Tyr Asn Asn Ile Met Thr
 100 105 110

Val Pro Ala Leu Pro Lys Ser Leu Ile Ser Leu Ser Leu Ser His Thr
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Asn Ile Leu Met Leu Asp Ser Ala Ser Leu Ala Gly Leu His Ala Leu
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Arg Phe Leu Phe Met Asp Gly Asn Cys Tyr Tyr Lys Asn Pro Cys Arg

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Thr	His	Leu	Ser	Leu	Lys	Tyr	Asn	Asn	Leu	Thr	Val	Val	Pro	Arg	Asn
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Leu	Pro	Ser	Ser	Leu	Glu	Tyr	Leu	Leu	Leu	Ser	Tyr	Asn	Arg	Ile	Val
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Lys	Leu	Ala	Pro	Glu	Asp	Leu	Ala	Asn	Leu	Thr	Ala	Leu	Arg	Val	Leu
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Asp	Val	Gly	Gly	Asn	Cys	Arg	Arg	Cys	Asp	His	Ala	Pro	Asn	Pro	Cys
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Met	Glu	Cys	Pro	Arg	His	Phe	Pro	Gln	Leu	His	Pro	Asp	Thr	Phe	Ser
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His	Leu	Ser	Arg	Leu	Glu	Gly	Leu	Val	Leu	Lys	Asp	Ser	Ser	Leu	Ser
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Trp	Leu	Asn	Ala	Ser	Trp	Phe	Arg	Gly	Leu	Gly	Asn	Leu	Arg	Val	Leu
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Asp	Leu	Ser	Glu	Asn	Phe	Leu	Tyr	Lys	Cys	Ile	Thr	Lys	Thr	Lys	Ala
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Phe	Gln	Gly	Leu	Thr	Gln	Leu	Arg	Lys	Leu	Asn	Leu	Ser	Phe	Asn	Tyr
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Gln	Lys	Arg	Val	Ser	Phe	Ala	His	Leu	Ser	Leu	Ala	Pro	Ser	Phe	Gly
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Ser	Leu	Val	Ala	Leu	Lys	Glu	Leu	Asp	Met	His	Gly	Ile	Phe	Phe	Arg
			340					345					350		
Ser	Leu	Asp	Glu	Thr	Thr	Leu	Arg	Pro	Leu	Ala	Arg	Leu	Pro	Met	Leu
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Gln	Thr	Leu	Arg	Leu	Gln	Met	Asn	Phe	Ile	Asn	Gln	Ala	Gln	Leu	Gly
		370				375					380				
Ile	Phe	Arg	Ala	Phe	Pro	Gly	Leu	Arg	Tyr	Val	Asp	Leu	Ser	Asp	Asn
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Arg	Ile	Ser	Gly	Ala	Ser	Glu	Leu	Thr	Ala	Thr	Met	Gly	Glu	Ala	Asp
				405					410					415	
Gly	Gly	Glu	Lys	Val	Trp	Leu	Gln	Pro	Gly	Asp	Leu	Ala	Pro	Ala	Pro
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Val	Asp	Thr	Pro	Ser	Ser	Glu	Asp	Phe	Arg	Pro	Asn	Cys	Ser	Thr	Leu

435

440

445

Asn Phe Thr Leu Asp Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro
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Glu Met Phe Ala Gln Leu Ser His Leu Gln Cys Leu Arg Leu Ser His
 465 470 475 480

Asn Cys Ile Ser Gln Ala Val Asn Gly Ser Gln Phe Leu Pro Leu Thr
 485 490 495

Gly Leu Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His
 500 505 510

Glu His Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser
 515 520 525

Tyr Asn Ser Gln Pro Phe Gly Met Gln Gly Val Gly His Asn Phe Ser
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Phe Val Ala His Leu Arg Thr Leu Arg His Leu Ser Leu Ala His Asn
 545 550 555 560

Asn Ile His Ser Gln Val Ser Gln Gln Leu Cys Ser Thr Ser Leu Arg
 565 570 575

Ala Leu Asp Phe Ser Gly Asn Ala Leu Gly His Met Trp Ala Glu Gly
 580 585 590

Asp Leu Tyr Leu His Phe Phe Gln Gly Leu Ser Gly Leu Ile Trp Leu
 595 600 605

Asp Leu Ser Gln Asn Arg Leu His Thr Leu Leu Pro Gln Thr Leu Arg
 610 615 620

Asn Leu Pro Lys Ser Leu Gln Val Leu Arg Leu Arg Asp Asn Tyr Leu
 625 630 635 640

Ala Phe Phe Lys Trp Trp Ser Leu His Phe Leu Pro Lys Leu Glu Val
 645 650 655

Leu Asp Leu Ala Gly Asn Gln Leu Lys Ala Leu Thr Asn Gly Ser Leu
 660 665 670

Pro Ala Gly Thr Arg Leu Arg Arg Leu Asp Val Ser Cys Asn Ser Ile
 675 680 685

Ser Phe Val Ala Pro Gly Phe Phe Ser Lys Ala Lys Glu Leu Arg Glu
 690 695 700

Leu Asn Leu Ser Ala Asn Ala Leu Lys Thr Val Asp His Ser Trp Phe
 705 710 715 720

Gly Pro Leu Ala Ser Ala Leu Gln Ile Leu Asp Val Ser Ala Asn Pro
725 730 735

Leu His Cys Ala Cys Gly Ala Ala Phe Met Asp Phe Leu Leu Glu Val
740 745 750

Gln Ala Ala Val Pro Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro
755 760 765

Gly Gln Leu Gln Gly Leu Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys
770 775 780

Leu Asp Glu Ala Leu Ser Trp Asp Cys Phe Ala Leu Ser Leu Leu Ala
785 790 795 800

Val Ala Leu Gly Leu Gly Val Pro Met Leu His His Leu Cys Gly Trp
805 810 815

Asp Leu Trp Tyr Cys Phe His Leu Cys Leu Ala Trp Leu Pro Trp Arg
820 825 830

Gly Arg Gln Ser Gly Arg Asp Glu Asp Ala Leu Pro Tyr Asp Ala Phe
835 840 845

Val Val Phe Asp Lys Thr Gln Ser Ala Val Ala Asp Trp Val Tyr Asn
850 855 860

Glu Leu Arg Gly Gln Leu Glu Glu Cys Arg Gly Arg Trp Ala Leu Arg
865 870 875 880

Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly Lys Thr Leu Phe Glu
885 890 895

Asn Leu Trp Ala Ser Val Tyr Gly Ser Arg Lys Thr Leu Phe Val Leu
900 905 910

Ala His Thr Asp Arg Val Ser Gly Leu Leu Arg Ala Ser Phe Leu Leu
915 920 925

Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp Val Val Val Leu Val
930 935 940

Ile Leu Ser Pro Asp Gly Arg Arg Ser Arg Tyr Val Arg Leu Arg Gln
945 950 955 960

Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro His Gln Pro Ser Gly
965 970 975

Gln Arg Ser Phe Trp Ala Gln Leu Gly Met Ala Leu Thr Arg Asp Asn
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 Mus musculus

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ctg gca agt tcc ttt aag aac ctg gtg tca ctg cag gag ctg aac atg 96
 Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu Leu Asn Met
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aac ggc atc ttc ttc cgc ttg ctc aac aag tac acg ctc aga tgg ctg 144
 Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Tyr Thr Leu Arg Trp Leu
 35 40 45

gcc gat ctg ccc aaa ctc cac act ctg cat ctt caa atg aac ttc atc 192
 Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met Asn Phe Ile
 50 55 60

aac cag gca cag ctc agc atc ttt ggt acc ttc cga gcc ctt cgc ttt 240
 Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala Leu Arg Phe
 65 70 75 80

gtg gac ttg tca gac aat cgc atc agt ggg cct tca acg ctg tca gaa 288
 Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr Leu Ser Glu
 85 90 95

gcc acc cct gaa gag gca gat gat gca gag cag gag gag ctg ttg tct 336
 Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu Leu Leu Ser
 100 105 110

gcg gat cct cac cca gct ccg ctg agc acc cct gct tct aag aac ttc 384
 Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser Lys Asn Phe
 115 120 125

atg gac agg tgt aag aac ttc aag ttc aac atg gac ctg tct cgg aac 432
 Met Asp Arg Cys Lys Asn Phe Lys Phe Asn Met Asp Leu Ser Arg Asn
 130 135 140

aac ctg gtg act atc aca gca gag atg ttt gta aat ctc tca cgc ctc 480
 Asn Leu Val Thr Ile Thr Ala Glu Met Phe Val Asn Leu Ser Arg Leu

145	150	155	160	
cag tgt ctt agc ctg agc cac aac tca att gca cag gct gtc aat ggc				528
Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala Val Asn Gly	165	170	175	
tct cag ttc ctg ccg ctg acc ggt ctg cag gtg cta gac ctg tcc cac				576
Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu Ser His	180	185	190	
aat aag ctg gac ctc tac cac gag cac tca ttc acg gag cta cca cga				624
Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu Pro Arg	195	200	205	
ctg gag gcc ctg gac ctc agc tac aac agc cag ccc ttt agc atg aag				672
Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Lys	210	215	220	
ggt ata ggc cac aat ttc agt ttt gtg acc cat ctg tcc atg cta cag				720
Gly Ile Gly His Asn Phe Ser Phe Val Thr His Leu Ser Met Leu Gln	225	230	235	240
agc ctt agc ctg gca cac aat gac att cat acc cgt gtg tcc tca cat				768
Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val Ser Ser His	245	250	255	
ctc aac agc aac tca gtg agg ttt ctt gac ttc agc ggc aac ggt atg				816
Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly Asn Gly Met	260	265	270	
ggc cgc atg tgg gat gag ggg ggc ctt tat ctc cat ttc ttc caa ggc				864
Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe Phe Gln Gly	275	280	285	
ctg agt ggc gtg ctg aag ctg gac ctg tct caa aat aac ctg cat atc				912
Leu Ser Gly Val Leu Lys Leu Asp Leu Ser Gln Asn Asn Leu His Ile	290	295	300	
ctc cgg ccc cag aac ctt gac aac ctc ccc aag agc ctg aag ctg ctg				960
Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu Lys Leu Leu	305	310	315	320
agc ctc cga gac aac tac cta tct ttc ttt aac tgg acc agt ctg tcc				1008
Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr Ser Leu Ser	325	330	335	
ttc cta ccc aac ctg gaa gtc cta gac ctg gca ggc aac cag cta aag				1056
Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn Gln Leu Lys	340	345	350	
gcc ctg acc aat ggc acc ctg cct aat ggc acc ctc ctc cag aaa ctc				1104
Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu Gln Lys Leu	355	360	365	

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aag	gcc	aag	gag	ctg	cga	gag	ctc	aac	ctt	agc	gcc	aac	gcc	ctc	aag	1200
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Thr	Val	Asp	His	Ser	Trp	Phe	Gly	Pro	Ile	Val	Met	Asn	Leu	Thr	Val	
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cta	gac	gtg	aga	agc	aac	cct	ctg	cac	tgt	gcc	tgt	ggg	gca	gcc	ttc	1296
Leu	Asp	Val	Arg	Ser	Asn	Pro	Leu	His	Cys	Ala	Cys	Gly	Ala	Ala	Phe	
			420					425					430			
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Ala	Gln	Asp	Leu	Arg	Leu	Cys	Leu	Asp	Glu	Val	Leu	Ser	Trp	Asp	Cys	
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Phe	Gly	Leu	Ser	Leu	Leu	Ala	Val	Ala	Val	Gly	Met	Val	Val	Pro	Ile	
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Leu	His	His	Leu	Cys	Gly	Trp	Asp	Val	Trp	Tyr	Cys	Phe	His	Leu	Cys	
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Leu	Ala	Trp	Leu	Pro	Leu	Leu	Ala	Arg	Ser	Arg	Arg	Ser	Ala	Gln	Thr	
		515					520					525				
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Leu	Pro	Tyr	Asp	Ala	Phe	Val	Val	Phe	Asp	Lys	Ala	Gln	Ser	Ala	Val	
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gcc	gac	tgg	gtg	tat	aac	gag	ctg	cgg	gtg	cgg	ctg	gag	gag	cgg	cgc	1680
Ala	Asp	Trp	Val	Tyr	Asn	Glu	Leu	Arg	Val	Arg	Leu	Glu	Glu	Arg	Arg	
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Lys	Thr	Leu	Phe	Val	Leu	Ala	His	Thr	Asp	Arg	Val	Ser	Gly	Leu	Leu				
		595					600					605							
cgc	acc	agc	ttc	ctg	ctg	gct	cag	cag	cgc	ctg	ttg	gaa	gac	cgc	aag	1872			
Arg	Thr	Ser	Phe	Leu	Leu	Ala	Gln	Gln	Arg	Leu	Leu	Glu	Asp	Arg	Lys				
	610					615					620								
gac	gtg	gtg	gtg	ttg	gtg	atc	ctg	cgt	ccg	gat	gcc	cac	cgc	tcc	cgc	1920			
Asp	Val	Val	Val	Leu	Val	Ile	Leu	Arg	Pro	Asp	Ala	His	Arg	Ser	Arg				
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Tyr	Val	Arg	Leu	Arg	Gln	Arg	Leu	Cys	Arg	Gln	Ser	Val	Leu	Phe	Trp				
				645					650					655					
ccc	cag	cag	ccc	aac	ggg	cag	ggg	ggc	ttc	tgg	gcc	cag	ctg	agt	aca	2016			
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gcc	ctg	act	agg	gac	aac	cgc	cac	ttc	tat	aac	cag	aac	ttc	tgc	cgg	2064			
Ala	Leu	Thr	Arg	Asp	Asn	Arg	His	Phe	Tyr	Asn	Gln	Asn	Phe	Cys	Arg				
		675					680					685							
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 Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Tyr Thr Leu Arg Trp Leu
 35 40 45
 Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met Asn Phe Ile

50

55

60

Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala Leu Arg Phe
65 70 75 80

Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr Leu Ser Glu
85 90 95

Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu Leu Leu Ser
100 105 110

Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser Lys Asn Phe
115 120 125

Met Asp Arg Cys Lys Asn Phe Lys Phe Asn Met Asp Leu Ser Arg Asn
130 135 140

Asn Leu Val Thr Ile Thr Ala Glu Met Phe Val Asn Leu Ser Arg Leu
145 150 155 160

Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala Val Asn Gly
165 170 175

Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu Ser His
180 185 190

Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu Pro Arg
195 200 205

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Lys
210 215 220

Gly Ile Gly His Asn Phe Ser Phe Val Thr His Leu Ser Met Leu Gln
225 230 235 240

Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val Ser Ser His
245 250 255

Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly Asn Gly Met
260 265 270

Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe Phe Gln Gly
275 280 285

Leu Ser Gly Val Leu Lys Leu Asp Leu Ser Gln Asn Asn Leu His Ile
290 295 300

Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu Lys Leu Leu
305 310 315 320

Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr Ser Leu Ser
325 330 335

Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn Gln Leu Lys
 340 345 350
 Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu Gln Lys Leu
 355 360 365
 Asp Val Ser Ser Asn Ser Ile Val Ser Val Ala Pro Gly Phe Phe Ser
 370 375 380
 Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys
 385 390 395 400
 Thr Val Asp His Ser Trp Phe Gly Pro Ile Val Met Asn Leu Thr Val
 405 410 415
 Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe
 420 425 430
 Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly Leu Ala Asn
 435 440 445
 Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe
 450 455 460
 Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser Trp Asp Cys
 465 470 475 480
 Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val Val Pro Ile
 485 490 495
 Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe His Leu Cys
 500 505 510
 Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser Ala Gln Thr
 515 520 525
 Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val
 530 535 540
 Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg Arg
 545 550 555 560
 Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp Trp Leu Pro
 565 570 575
 Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr Gly Ser Arg
 580 585 590
 Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu
 595 600 605
 Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys
 610 615 620

Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His Arg Ser Arg
525 630 635 640

Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Phe Trp
645 650 655

Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln Leu Ser Thr
660 665 670

Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln Asn Phe Cys Arg
675 680 685

Gly Pro Thr Ala Glu
690

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